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(54) Title: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE THEREOF		
(57) Abstract The present invention provides a novel family of apoptosis-modulating proteins. Nucleotide and amino acid residue sequences, derivatives thereof and methods of use thereof are also provided.		

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NOVEL APOPTOSIS-MODULATING PROTEINS, DNA ENCODING
THE PROTEINS AND METHODS OF USE THEREOF

This is a continuation-in-part of United States patent application Serial No. 08/320,157 which is a
5 continuation-in-part of United States patent application Serial No. 08/160,067 filed November 30, 1993.

Field of the Invention

This invention relates to novel proteins with apoptosis-modulating activity, recombinant DNA encoding
10 the proteins, compositions containing the proteins and methods of use thereof.

Background of the Invention

Apoptosis is a normal physiologic process that leads to individual cell death. This process of programmed
15 cell death is involved in a variety of normal and pathogenic biological events and can be induced by a number of unrelated stimuli. Changes in the biological regulation of apoptosis also occur during aging and are responsible for many of the conditions and diseases
20 related to aging. Recent studies of apoptosis have implied that a common metabolic pathway leading to cell death may be initiated by a wide variety of signals, including hormones, serum growth factor deprivation, chemotherapeutic agents, ionizing radiation and infection
25 by human immunodeficiency virus (HIV). Wyllie (1980) Nature 284:555-556; Kanter et al. (1984) Biochem. Biophys. Res. Commun. 118:392-399; Duke and Cohen (1986) Lymphokine Res. 5:289-299; Tomei et al. (1988) Biochem. Biophys. Res. Commun. 155:324-331; Kruman et al. (1991)
30 J. Cell. Physiol. 148:267-273; Ameisen and Capron (1991) Immunology Today 12:102; and Sheppard and Ascher (1992) J. AIDS 5:143. Agents that modulate the biological control of apoptosis thus have therapeutic utility in a wide variety of conditions.

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Apoptotic cell death is characterized by cellular shrinkage, chromatin condensation, cytoplasmic blebbing, increased membrane permeability and internucleosomal DNA cleavage. Kerr et al. (1992) FASEB J. 6:2450; and Cohen and Duke (1992) Ann. Rev. Immunol. 10:267. The blebs, small, membrane-encapsulated spheres that pinch off of the surface of apoptotic cells, may continue to produce superoxide radicals which damage surrounding cell tissue and may be involved in inflammatory processes.

10 Bcl-2 was discovered at the common chromosomal translocation site t(14:18) in follicular lymphomas which results in aberrant over-expression of bcl-2. Tsujimoto et al. (1984) Science 226:1097-1099; and Cleary et al. (1986) Cell 47:19-28. The normal function of bcl-2 is
15 the prevention of apoptosis; unregulated expression of bcl-2 in B cells is thought to lead to increased numbers of proliferating B cells which may be a critical factor in the development of lymphoma. McDonnell and Korsmeyer (1991) Nature 349:254-256; and, for review see, Edgington
20 (1993) Bio/Tech. 11:787-792. Bcl-2 is also capable of blocking γ irradiation-induced cell death. Sentman et al. (1991) Cell 67:879-888; and Strasser (1991) Cell 67:889-899. It is now known that bcl-2 inhibits most types of apoptotic cell death and is thought to function
25 by regulating an antioxidant pathway at sites of free radical generation and Ca^{++} flux through the endoplasmic reticulum. Lan et al. (1984) Proc. Natl. Acad. Sci. 91:6569-6573; Hockenbery et al. (1993) Cell 75:241-251.

While apoptosis is a normal cellular event, it can
30 also be induced by pathological conditions and a variety of injuries. Apoptosis is involved in a wide variety of conditions including, but not limited to, cardiovascular disease; cancer regression; immunoregulation; viral diseases; anemia; neurological disorders;
35 gastrointestinal disorders, including but not limited to, diarrhea and dysentery; diabetes; hair loss; rejection of

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organ transplants; prostate hypertrophy; obesity; ocular disorders; stress; and aging.

Bcl-2 belongs to a family of proteins some of which have been cloned and sequenced. Williams and Smith
5 (1993) Cell 74:777-779. All references cited herein, both supra and infra, are hereby incorporated by reference herein.

Summary of the Invention

Substantially purified DNA encoding novel *Bcl-2*
10 homologs, termed *Cdn-1*, *Cdn-2* and *Cdn-3* and derivatives thereof, as well as recombinant cells and transgenic animals expressing the *Cdn-1* and *Cdn-2* nucleotides are provided. The substantially purified *Cdn-1* and *Cdn-2* proteins and compositions thereof are also provided.
15 Diagnostic and therapeutic methods utilizing the nucleotides and proteins are also provided. Methods of screening for pharmaceutical agents that stimulate, as well as pharmaceutical agents that modulate *Cdn-1* and *Cdn-2* expression and protein activity and interactions
20 are also provided. Methods of screening for proteins that interact with *Cdns* are also provided.

Brief description of the Drawings

Figure 1 depicts the *Bcl-2* family PCR primers used to isolate the *Cdn-1* probes.

25 Figure 2 depicts the *Cdn-1* clones obtained by the methods described in Example 1.

Figure 3 depicts the nucleotide sequence of *Cdn-1* cDNA and encoded amino acid sequence of the *Cdn-1* protein.

30 Figure 4 depicts the results of a Northern blot analysis of multiple tissues with probes specific for both *Bcl-2* and *Cdn-1*.

Figure 5 shows the sequence of the *Cdn-2* gene and flanking sequences and the corresponding predicted amino
35 acid sequence of the *Cdn-2* protein.

Figure 6 shows a comparison of the N-terminal amino acid sequences of *Cdn-1*, *Cdn-2* and known *Bcl-2* family members.

Figure 7 shows the nucleotide sequence of the *Cdn-3* gene and predicted amino acid sequence of the *Cdn-3* protein.

Figure 8 shows the anti-apoptotic effects of *Cdn-1* and some of its derivatives in serum-deprivation induced apoptosis of WI-L2 transformants in 0.1% FBS.

Figure 9 (response of WI-L2 transformants to anti-Fas-Induced Apoptosis (50 ng/mL anti-FAS)) shows anti-apoptotic effects of *Cdn-1* and some of its derivatives in FAS-induced apoptosis of WI-L2 cells.

Figure 10 shows modulation of apoptosis by *Cdn-1* and *Cdn-2* in FL5.12 cells.

Figure 11 depicts the *Cdn-1* derivative proteins $\Delta 1$, $\Delta 2$ and $\Delta 3$. The N-terminal residues are indicated by the arrows. The remainder of the derivative proteins is the same as full-length *Cdn-1*.

Detailed Description of the Invention

The present invention encompasses substantially purified nucleotide sequences encoding the novel *Bcl-2* homologs, *Cdn-1* and *Cdn-2*; and the proteins encoded thereby; compositions comprising *Cdn-1* and *Cdn-2* nucleotides, and proteins and methods of use of thereof. Note that in copending United States patent application Serial No. 08/160,067, *Cdn-1* was termed *cdi-1* and that in copending United States Patent application Serial No. 08/320,157 *Cdn* was termed *cdn* and *Cdn* was termed *CDN*; although the names have been changed, the nucleotide and amino acid sequences remain identical. The invention further includes recombinant cells and transgenic animals expressing the cloned *Cdn-1* or *Cdn-2* genes. The nucleotide and predicted amino acid residue sequences encoded by *Cdn-1* are shown in Figure 3; and those of *Cdn-2* are shown in Figure 5. It has now been found that the proteins encoded by the *Cdn* genes are capable of

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modulating apoptosis. In an Epstein-Barr Virus (EBV) transformant lymphoblastoid cell line, *Cdn-1* was shown to decrease Fas-mediated apoptosis. In a mouse progenitor B cell line, FL5.12, expression of *Cdn-2* and a derivative of *Cdn-1* decrease IL-3-induced apoptosis whereas expression of *Cdn-1* slightly increased apoptosis. Thus, depending on the cell type, the derivative or type of *Cdn* expressed and the method of induction of apoptosis, apoptosis can be modulated in a highly specific manner by controlling the expression of *Cdns* and concentration of *Cdns*.

As used herein, "*Cdns*" or "*Cdn*" refers to the nucleic acid molecules (nucleotides) described herein (*Cdn-1*, *Cdn-2*, *Cdn-3* and derivatives thereof), "*the Cdns*" or "*Cdn*" refers to the proteins encoded thereby (*Cdn-1*, *Cdn-2*, *Cdn-3* and derivatives thereof). The present invention encompasses *Cdn-1* and *Cdn-2* nucleotide sequences. The nucleotides include, but are not limited to, the *Cdn-1* cDNA, genome-derived DNA and synthetic or semi-synthetic nucleotides such as DNA, and RNA both coding and complementary to the coding region. The nucleotides may be complementary to the mRNA for at least a fragment of the *Cdns* and other nucleotides which can bind to either the DNA or mRNA encoding the *Cdns*. These complementary nucleotides include, but are not limited to, nucleotides capable of forming triple helices and antisense nucleotides. The complementary nucleotides may be expressed endogenously by one of the vectors described herein or may be added exogenously by methods known in the art of oligonucleotide therapy. Reed et al. (1990) Cancer Res. 50:6565-6570. The nucleotide sequence of the *Cdn-1* cDNA with the location of restriction endonuclease sites is shown in Figure 4. As described in the examples herein, *Cdn-1* mRNA has been detected in a variety of human organs and tissues by Northern blot analysis. These organs include liver; heart; skeletal muscle; lung; kidney; and pancreas as shown in Figure 3.

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Similarly, *Cdn-2* cDNA, genomic DNA and synthetic or semi-synthetic nucleotides are additional embodiments of the present invention. The nucleotide sequence of the *Cdn-2* gene, along with the predicted amino acid sequence of *Cdn-2* protein and the locations of restriction endonuclease recognition sites, is given in Figure 5.

The examples presented herein indicate that *Cdn-1* is on human chromosome 6 and that *Cdn-2* is on human chromosome 20. There is also a member of the family *Cdn-3* which is on human chromosome 11. Fluorescence in situ hybridization (FISH) indicated an approximate location of *Cdn-1* to be at 6p21-23. It is possible that *Cdn-2* and *Cdn-3* are pseudogenes. While these may not be expressed endogenously, they are capable of being expressed from a recombinant vector providing the appropriate promoter sequences. Thus, both *Cdn-2* and *Cdn-3* nucleotide sequences are encompassed by the present invention as are recombinant constructs thereof and proteins encoded thereby.

Derivatives of the genes and proteins include any portion of the protein, or nucleotide sequence encoding the protein, which retains apoptosis modulating activity. Figure 11 depicts three such derivatives of *Cdn-1* which have been shown to retain apoptosis-modulating activity. The derivatives, *Cdn1-Δ1*, *Cdn1-Δ2* and *Cdn1-Δ3*, and the proteins encoded thereby are encompassed by the present invention.

The invention includes modifications to *Cdn* DNA sequences such as deletions, substitutions and additions particularly in the non-coding regions of genomic DNA. Such changes are useful to facilitate cloning and modify gene expression.

The invention further encompasses various substituted nucleotides. Substitutions can be made within the coding region that either do not alter the amino acid residues encoded or result in conservatively substituted amino acid residues. Nucleotide

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substitutions that do not alter the amino acid residues encoded are useful for optimizing gene expression in different systems. Suitable substitutions are known to those of skill in the art and are made, for instance, to reflect preferred codon usage in the particular expression systems.

The invention encompasses functionally equivalent variants and derivatives of Cdns which may enhance, decrease or not significantly affect the properties of Cdns. For instance, changes in the DNA sequence that do not change the encoded amino acid sequence, as well as those that result in conservative substitutions of amino acid residues, one or a few amino acid deletions or additions, and substitution of amino acid residues by amino acid analogs are those which will not significantly affect its properties.

Amino acid residues which can be conservatively substituted for one another include but are not limited to: glycine/alanine; valine/isoleucine/leucine; asparagine/glutamine; aspartic acid/glutamic acid; serine/threonine; lysine/arginine; and phenylalanine/tyrosine. Any conservative amino acid substitution which does not significantly affect the properties of Cdns is encompassed by the present invention.

The invention further encompasses mutants of Cdns which, when expressed, interfere with the activity of endogenously expressed Cdns. Such mutants can be made by any method known in the art and screened for activity by their ability to affect activity of native Cdns.

Techniques for nucleic acid manipulation useful for the practice of the present invention are known in the art and described in a variety of references, including, but not limited to, Molecular Cloning: A Laboratory Manual, 2nd ed., vols. 1-3, eds. Sambrook et al. Cold Spring Harbor Laboratory Press (1989); and Current Protocols in Molecular Biology, eds. Ausubel et al.,

Greene Publishing and Wiley-Interscience: New York (1987) and periodic updates.

The invention further embodies a variety of DNA vectors having cloned therein the *Cdn* nucleotide sequences. Suitable vectors include any known in the art including, but not limited to, those for use in bacterial, mammalian, yeast and insect expression systems. Specific vectors are known in the art and need not be described in detail herein.

10 The vectors may also provide inducible promoters for expression of the *Cdn* nucleotide sequences. Inducible promoters are those which do not allow substantial constitutive expression of the gene but rather, permit expression only under certain circumstances. Such
15 promoters may be induced by a variety of stimuli including, but not limited to, exposure of a cell containing the vector to a ligand, metal ion, other chemical or change in temperature. The promoters may also be cell-specific, that is, inducible only in a
20 particular cell type and often only during a specific period of time. The promoter may further be cell cycle specific, that is, induced or inducible only during a particular stage in the cell cycle. The promoter may be both cell type specific and cell cycle specific. Any
25 inducible or noninducible promoter known in the art is suitable for use in the present invention. Preferably, the promoter used is inducible.

The invention further includes a variety of expression systems transfected with the vectors.

30 Suitable expression systems include, but are not limited to, bacterial, mammalian, yeast and insect. Specific expression systems and the use thereof are known in the art and are not described in detail herein.

The invention encompasses *ex vivo* transfection with
35 *Cdn* nucleotide sequences, in which cells removed from animals including man are transfected with vectors containing *Cdn* nucleotides and reintroduced into animals.

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Suitable transfected cells include individual cells or cells contained within whole tissues. In addition, *ex vivo* transfection can include the transfection of cells derived from an animal other than the animal or human subject into which the cells are ultimately introduced. Such grafts include, but are not limited to, allografts, xenografts, and fetal tissue transplantation. In addition, *in vivo* transfection such as by pulmonary administration of suitable vectors can be used.

Essentially any cell or tissue type can be treated in this manner. Suitable cells include, but are not limited to, cardiomyocytes and lymphocytes. For instance, lymphocytes, removed, transfected with the recombinant DNA and reintroduced into an HIV-positive patient may increase the half-life of the reintroduced T cells.

As an example, in treatment of HIV-infected patients by the above-described method, the white blood cells are removed from the patient and sorted to yield the CD4⁺ cells. The CD4⁺ cells are then transfected with a vector containing a *Cdn* nucleotide and reintroduced into the patient. Alternatively, the unsorted lymphocytes can be transfected with a recombinant vector having at least one *Cdn* nucleotide under the control of a cell-specific promoter such that only CD4⁺ cells express the nucleotides. In this case, an ideal promoter would be the CD4 promoter; however, any suitable CD4⁺ T cell-specific promoter can be used.

Further, the invention encompasses cells transfected *in vivo* by the vectors. Suitable methods of *in vivo* transfection are known in the art and include, but are not limited to, that described by Zhu et al. (1993) Science 261:209-211. *in vivo* transfection may be particularly useful as a prophylactic treatment for patients suffering from atherosclerosis. Modulation of the levels of *Cdn* could serve as prophylaxis for the apoptosis-associated reperfusion damage that results from

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cerebral and myocardial infarctions. In these patients with a high risk of stroke and heart attack, the apoptosis and reperfusion damage associated with arterial obstruction could be prevented or at least mitigated.

5 Infarctions are caused by a sudden insufficiency of arterial or venous blood supply due to emboli, thrombi, or pressure that produces a macroscopic area of necrosis; the heart, brain, spleen, kidney, intestine, lung and testes are likely to be affected. Apoptosis occurs to
10 tissues surrounding the infarct upon reperfusion of blood to the area; thus, modulation of *Cdn* levels, achieved by a biological modifier-induced change in endogenous production, by *in vivo* transfection or by anti-sense therapy, could be effective at reducing the severity of
15 damage caused by heart attacks and stroke.

Transgenic animals containing the recombinant DNA vectors containing *Cdn* nucleotide sequences are also encompassed by the invention. Methods of making transgenic animals are known in the art and need not be
20 described in detail herein. For a review of methods used to make transgenic animals, see, e.g., PCT publication no. WO 93/04169. Preferably, such animals express recombinant *Cdns* under control of a cell-specific and, even more preferably, a cell cycle-specific promoter.

25 In another embodiment, diagnostic methods are provided to detect the expression of *Cdns* either at the protein level or the mRNA level. Any antibody that specifically recognizes *Cdns* is suitable for use in *Cdn* diagnostics. Abnormal levels of *Cdns* are likely to be
30 found in the tissues of patients with diseases associated with inappropriate apoptosis; diagnostic methods are therefore useful for detecting and monitoring biological conditions associated with such apoptosis defects. Detection methods are also useful for monitoring the
35 success of *Cdn*-related therapies.

Purification or isolation of *Cdns* expressed either by the recombinant DNA or from biological sources such as

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tissues can be accomplished by any method known in the art. Protein purification methods are known in the art. Generally, substantially purified proteins are those which are free of other, contaminating cellular substances, particularly proteins. Preferably, the purified Cdns are more than eighty percent pure and most preferably more than ninety-five percent pure. For clinical use as described below, the Cdns are preferably highly purified, at least about ninety-nine percent pure, and free of pyrogens and other contaminants.

Suitable methods of protein purification are known in the art and include, but are not limited to, affinity chromatography, immunoaffinity chromatography, size exclusion chromatography, HPLC and FPLC. Any purification scheme that does not result in substantial degradation of the protein is suitable for use in the present invention.

The invention also includes the substantially purified Cdns having the amino acid residue sequences depicted in Figures 3 and 5, respectively. The invention encompasses functionally equivalent variants of Cdns which do not significantly affect their properties and variants which retain the same overall amino acid sequence but which have enhanced or decreased activity. For instance, conservative substitutions of amino acid residues, one or a few amino acid deletions or additions, and substitution of amino acid residues by amino acid analogs are within the scope of the invention. Any conservative amino acid substitution which does not significantly affect the properties of Cdns is encompassed by the present invention.

Suitable antibodies are generated by using the Cdns as an antigen or, preferably, peptides encompassing the Cdn regions that lack substantial homology to the other gene products of the *Bcl-2* family. Methods of detecting proteins using antibodies and of generating antibodies

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using proteins or synthetic peptides are known in the art and are not described in detail herein.

Cdn protein expression can also be monitored by measuring the level of *Cdn* mRNA. Any method for
5 detecting specific mRNA species is suitable for use in this method. This is easily accomplished using the polymerase chain reaction (PCR). Preferably, the primers chosen for PCR correspond to the regions of the *Cdn* genes which lack substantial homology to other members of the
10 *Bcl* gene family. Alternatively, Northern blots can be utilized to detect *Cdn* mRNA by using probes specific to *Cdns*. Methods of utilizing PCR and Northern blots are known in the art and are not described in detail herein.

Methods of treatment with *Cdns* also include
15 modulating cellular expression of *Cdns* by increasing or decreasing levels of mRNA or protein. Suitable methods of modulating cellular expression of *Cdn* include, but are not limited to, increasing endogenous expression with biological modifiers; transfecting the cells with vectors
20 encoding *Cdn* nucleotides so that either a *Cdn* gene is overexpressed or an anti-sense nucleotide is expressed; and expressing mutant *Cdns* which interfere with the interaction of endogenous *Cdn* with other proteins such as other members of the *Bcl-2* family. Cellular transfection
25 is discussed above and is known in the art. Suitable indications for modulating endogenous levels of *Cdn* include, but are not limited to, malignancies and cardiac-specific expression. Cardiac specific expression is particularly suitable for use in indications
30 including, but not limited to, patients susceptible to heart disease and in advance of cardiotoxic therapies including, but not limited to, chemotherapies such as adriamycin, so as to offer cardioprotection.

Modulating endogenous expression of *Cdns* can be
35 accomplished by exposing the cells to biological modifiers that directly or indirectly change levels of *Cdns* either by modulating expression of *Cdns* or by

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modulating degradation of *Cdn* mRNA. Suitable biological modifiers include, but are not limited to, molecules and other cells. Suitable molecules include, but are not limited to, drugs, cytokines, small molecules, hormones, combinations of interleukins, lectins and other stimulating agents e.g., PMA, LPS, bispecific antibodies and other agents which modify cellular functions or protein expression. Preferably, a suitable biological modifier is γ IFN which increases *Cdn* expression levels in HT-29 cells. Further, biological modifiers include *Cdn* nucleotides which modify expression of endogenous *Cdn* and mutant *Cdns* which interfere with the activity of endogenous *Cdns*. Cells are exposed to such biological modifiers at physiologically effective concentrations, and the expression of *Cdns* is measured relative to a control not exposed to the biological modifiers. Those biological modifiers which change expression of *Cdns* relative to the control are selected for further study.

The methods of decreasing endogenous levels of *Cdns* include, but are not limited to, antisense nucleotide therapy and methods to deliver the sense on antisense construct and down-regulation of expression by biological modifiers. Antisense therapy is known in the art and its application will be apparent to one of skill in the art.

Screening for therapeutically effective biological modifiers is done either by exposing the cells to biological modifiers which may directly or indirectly modulate levels of *Cdns* either by changing expression or by altering the half-life of *Cdn* mRNA or *Cdns*. The biological modifiers may also interfere with *Cdn*-1 interactions with both other *Bcl*-2 family members, and other gene products, e.g., proteases. Suitable biological modifiers include, but are not limited to, molecules and other cells. Suitable molecules include, but are not limited to, drugs, cytokines, small molecules, hormones, combinations of interleukins, lectins and other stimulating agents, e.g., PMA, LPS,

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bispecific antibodies, *Cdn* nucleotides, *Cdn* mutants and other agents which modify cellular functions or protein expression. Cells are grown under conditions known to elicit expression of at least one *Cdn* (preferably *Cdn-1*),
5 exposed to such biological modifiers at physiologically effective concentrations, and the expression of *Cdns* is measured relative to a control not exposed to biological modifiers. Those biological modifiers which modulate the expression of *Cdns* relative to a control are selected for
10 further study. Cell viability is also monitored to ensure that altered *Cdn* expression is not due to cell death.

In determining the ability of biological modifiers to modulate (increase or decrease) *Cdn* expression, the
15 levels of endogenous expression may be measured or the levels of recombinant fusion proteins under control of *Cdn*-specific promoter sequences may be measured. The fusion proteins are encoded by reporter genes.

Reporter genes are known in the art and include, but
20 are not limited to chloramphenicol acetyl transferase (CAT) and β -galactosidase. Expression of *Cdn-1* and *Cdn-2* can be monitored as described above either by protein or mRNA levels. Expression of the reporter genes can be monitored by enzymatic assays, or antibody-based assays,
25 like ELISAs and RIAs, also known in the art. Potential pharmaceutical agents can be any therapeutic agent or chemical known to the art, or any uncharacterized compounds derived from natural sources such as fungal broths and plant extracts. Preferably, suitable
30 pharmaceutical agents are those lacking substantial cytotoxicity and carcinogenicity.

Suitable indications for modulating endogenous levels of *Cdns* are any in which *Cdn*-mediated apoptosis is involved. These include, but are not limited to, various
35 types of malignancies and other disorders resulting in uncontrolled cell growth such as eczema, or deficiencies

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in normal programmed cell death such as malignancies, including, but not limited to, B cell lymphomas.

The invention also encompasses therapeutic methods and compositions involving treatment of patients with biological modifiers to modulate expression of *Cdns*. Effective concentrations and dosage regimens may be empirically derived. Such derivations are within the skill of those in the art and depend on, for instance, age, weight and gender of the patient and type and severity of the disease. Alternatively, patients may be directly treated with either native or recombinant *Cdns*. The *Cdns* should be substantially pure and free of pyrogens. It is preferred that the recombinant *Cdns* be produced in a mammalian cell line so as to ensure proper glycosylation. *Cdns* may also be produced in an insect cell line.

For therapeutic compositions, a therapeutically effective amount of substantially pure *Cdn* or biological modifier or oligonucleotide that modulates the expression or activity thereof is suspended in a physiologically accepted buffer including, but not limited to, saline and phosphate buffered saline (PBS) and administered to the patient. Preferably administration is intravenous. Other methods of administration include but are not limited to, subcutaneous, intraperitoneal, gastrointestinal and directly to a specific organ, such as intracardiac, for instance, to treat cell death related to myocardial infarction.

Suitable buffers and methods of administration are known in the art. The effective concentration of a *Cdn* or biological modifier therefor will need to be determined empirically and will depend on the type and severity of the disease, disease progression and health of the patient. Such determinations are within the skill of one in the art.

Bcl-2 is thought to function in an antioxidant pathway. Veis et al. (1993) Cell 75:229-240. Therefore,

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therapy involving Cdns is suitable for use in conditions in which superoxide is involved. Administration of modulators of Cdn expression results in an increased extracellular concentration of Cdns, which is thought to provide a method of directly inhibiting superoxide accumulation that may be produced by the blebs associated with apoptosis. The therapeutic method thus includes, but is not limited to, inhibiting superoxide mediated cell injury.

10 Suitable indications for therapeutic use of Cdns or biological modifier therefor are those involving free radical mediated cell death and include, but are not limited to, conditions previously thought to be treatable by superoxide dismutase. Such indications include, but are not limited to, HIV infection, autoimmune diseases, cardiomyopathies, neuronal disorders, hepatitis and other liver diseases, osteoporosis, and shock syndromes, including, but not limited to, septicemia.

20 Hybridization of cloned Cdn DNA to messenger mRNA from various regions of the brain indicated high levels of expression of Cdn-1 in each of the regions studied (Figure 8). Therefore, neurological disorders are another area in which therapeutic applications of Cdns are indicated.

25 The invention further encompasses methods of assaying for interactions between Cdns and proteins which bind specifically to Cdns. The assays entail contacting purified Cdns with cell lysates containing a protein which may bind to Cdns under conditions sufficient for the protein to bind and assaying for the presence of the protein.

Typically the assay step involves contacting the protein with a specific binding partner such as an antibody which may be directly or indirectly labeled.

35 Suitable assays include an ELISA that provides antibodies directed against the protein, in vitro translated Cdn and cell lysates containing the protein. Yeast genetic

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systems such as the Matchmaker (Clontech) are also suitable for use in the assay.

The following examples are provided to illustrate but not limit the present invention. Unless otherwise specified, all cloning techniques were essentially as described by Sambrook et al. (1989) and all reagents were used according to the manufacturer's instructions.

Example 1

Identification and Cloning of Cdn-1 cDNA

10 An amino acid sequence comparison of the six known Bcl-2 family members (Figure 6) revealed two regions with considerable sequence identity, namely amino acids 144-150 and 191-199. In an attempt to identify new Bcl-2 family members, degenerate PCR primers based on sequences
15 in these regions were designed (Figure 1) and PCR was performed using human heart cDNA and human B lymphoblastoid cell line (WI-L2) cDNA. PCR was performed using the Hot Start/Ampliwax technique (Perkin Elmer Cetus). The final concentration of the PCR primers and
20 the template cDNA were 4 μ M and 0.1-0.2 ng/ml, respectively. The conditions for cDNA synthesis were identical to those for first strand cDNA synthesis of the cDNA library as described below. PCR was performed in a Perkin Elmer Cetus DNA Thermal Cycler according to the
25 method described by Kiefer et al. (1991) Biochem. Biophys. Res. Commun. 176:219-225, except that the annealing and extension temperatures during the first 10 cycles were 36°C. Following PCR, samples were treated with 5 units of DNA polymerase I, Klenow fragment for 30
30 min at 37°C and then fractionated by electrophoresis on a 7% polyacrylamide, 1 X TBE (Tris/borate/EDTA) gel. DNA migrating between 170-210 base pairs was excised from the gel, passively eluted for 16 hours with gentle shaking in 10 mM Tris-HCl pH 7.5, 1 mM EDTA (TE), purified by
35 passage over an Elutip-D column (Schleicher and Schuell), ligated to the pCR-Script vector (Stratagene) and

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transformed into *Escherichia coli* strain XL1-Blue MRF (Stratagene). Plasmid DNA from transformants (white colonies) containing both the heart and WI-L2 PCR products was isolated using the Magic Miniprep DNA Purification System (Promega), and the DNA inserts were sequenced by the dideoxy chain termination method according to Sanger et al. (1977) Proc. Natl. Acad. Sci. USA 74:5463-5467 (USB, Sequenase version 2.0). DNA sequence analysis of the eleven heart PCR products revealed two sequences identical to *Bcl-x* (Boise et al. (1993) Cell 74:597-608) and ten other sequences unrelated to the *Bcl-2* family.

DNA sequence analyses of the eleven WI-L2 PCR products yielded one *Bcl-x* sequence, five sequences identical to another *Bcl-2* family member, *bax* (Oldvai et al. (1993) Cell 74:609-619), four unrelated sequences and one novel *Bcl-2* related sequence, termed *Cdn-1*. The unique *Cdn-1* amino acid sequence encoded by the PCR product is shown in Figure 6 from amino acid 151-190 (top row).

To isolate the *Cdn-1* cDNA, a human heart cDNA library (Clontech) and a WI-L2 cDNA library, constructed as described by Zapf et al. (1990) J. Biol. Chem. 265:14892-14898 were screened using the *Cdn-1* PCR DNA insert as a probe. The DNA was ³²P-labeled according to the method described by Feinberg and Vogelstein (1984) Anal. Biochem. 137:266-267 and used to screen 150,000 recombinant clones from both libraries according to the method described by Kiefer et al. (1991). Eight positive clones were obtained from the WI-L2 cDNA library. Four clones from the WI-L2 cDNA library and two from the heart cDNA library were further purified and plasmid DNA containing the cDNA inserts was excised from the λ ZAPII vector (Stratagene) (Figure 2). The two longest clones, W7 (2.1 kb) and W5 (2.0 kb) were sequenced and shown to contain the *Cdn-1* probe sequence, thus confirming their authenticity. Two clones from the heart cDNA library

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were purified. The cDNA was subcloned into pBlsc and sequenced. The heart cDNAs also encoded *Cdn-1*.

The W7 DNA sequence along with the deduced amino acid residue sequence is shown in Figure 3. The deduced amino acid sequence of *Cdn-1* was also aligned for maximum sequence identity with the other *Bcl-2* family members and is shown in Figure 6. As can be seen, there is considerable sequence identity between *Cdn-1* and other family members between amino acids 100 and 200. Beyond this central region, sequence conservation falls off sharply. Like *Bcl-2*, *Cdn-1* appears to be an intracellular protein in that it does not contain either a hydrophobic signal peptide or N-linked glycosylation sites. *Cdn-1* does contain a hydrophobic C-terminus that is also observed with all *Bcl-2* family members except LMW5-HL, suggesting its site of anti-apoptotic activity, like that of *Bcl-2*, is localized to a membrane bound organelle such as the mitochondrial membrane, the endoplasmic reticulum or the nuclear membrane.

Hockenbery et al. (1990); Chen-Levy et al. (1989) Mol. Cell. Biol. 9:701-710; Jacobsen et al. (1993) Nature 361:365-369; and Monighan et al. (1992) J. Histochem. Cytochem. 40:1819-1825.

Example 2

Northern Blot Analysis of cDNA Clones

Northern blot analysis was performed according to the method described by Lehrach et al. (1977) Biochem. 16:4743-4651 and Thomas (1980) Proc. Natl. Acad. Sci. USA 77:5201-5205. In addition, a human multiple tissue Northern blot was purchased from Clontech. The coding regions of *Bcl-2* and *Cdn-1* cDNAs were labeled by the random priming method described by Feinberg and Vogelstein (1984) Anal. Biochem. 137:266-267. Hybridization and washing conditions were performed according to the methods described by Kiefer et al. (1991). Specifically, Klenow-labeled fragments of *Bcl-2*

-20-

and *Cdn-1* clones were hybridized to a multiple human tissue Northern blot (Clontech 7760-1), at a final concentration of 1×10^6 cpm/milliliter for each probe. The blot was washed at high stringency.

- 5 The results, presented in Figure 4 indicate that *Cdn-1* is expressed in all organs tested (heart, brain, placenta, lung, liver, skeletal muscle, kidney and pancreas) whereas *Bcl-2* is not expressed or expressed at only low levels in heart, brain, lung, and liver. Thus,
- 10 *Cdn-1* appears to be more widely expressed throughout human organs than *Bcl-2* and may be more important in regulating apoptosis in these tissues.

Example 3

Expression of Recombinant *Cdn-1*

- 15 In order to express recombinant *Cdn-1* in the baculovirus system, the *Cdn-1* cDNA generated in Example 1 was used to generate a novel *Cdn-1* vector, by a PCR methodology as described in Example 1, using primers from the 3' and 5' flanking regions of the gene which contain
- 20 restriction sites to facilitate cloning. The plasmids were sequenced by the dideoxy terminator method (Sanger et al., 1977) using sequencing kits (USB, Sequenase version 2.0) and internal primers. This was to confirm that no mutations resulted from PCR.

- 25 A clone was used to generate recombinant viruses by *in vivo* homologous recombination between the overlapping sequences of the plasmid and AcNPV wild type baculovirus. After 48 hours post-transfection in insect *Spodoptera frugiperda* clone 9 (SF9) cells, the recombinant viruses
- 30 were collected, identified by PCR and further purified. Standard procedures for selection, screening and propagation of recombinant baculovirus were performed (Invitrogen). The molecular mass, on sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE), of
- 35 the protein produced in the baculovirus system was

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compared with the predicted molecular mass of Cdn-1 according to the amino-acid sequence.

In addition, similar clones can be expressed preferably in a yeast intracellular expression system by any method known in the art, including the method described by Barr et al. (1992) Transgenesis ed. JAH Murray, (Wiley and Sons) pp. 55-79.

Example 4

Expression of Cdn-1 in Mammalian Systems

10 The Cdn-1 coding sequence was excised from the plasmid generated in Example 1, and introduced into plasmids pCEP7, pREP7 and pCDNA3 (Invitrogen) at compatible restriction enzyme sites. pCEP7 was generated by removing the RSV 3'-LTR of pREP7 with XbaI/Asp718, and
15 substituting the CMV promoter from pCEP4 (Invitrogen). 25 µg of each Cdn-1-containing plasmid was electroporated into the B lymphoblastoid cell line WI-L2, and stable hygromycin resistant transformants or G418 resistant transformants (pCDNA3 constructs, Fig. 8) expressing
20 Cdn-1 were selected.

The coding region of Cdns can also be ligated into expression vectors capable of stably integrating into other cell types including, but not limited to, cardiomyocytes, neural cell lines such as GTI-7 and TNF
25 sensitive cells such as the human colon adenocarcinoma cell line HT29 so as to provide a variety of assay systems to monitor the regulation of apoptosis by Cdn-1.

Example 5

30 Effect of the Anti-Apoptotic Activity of Cdn-1 and its Derivatives in the Wild Type B Lymphoblastoid Cell Line WI-L2-729 HF2 and the Transformed Cell Expressing Excess Cdn-1

2x10⁵ WI-L2, and WI-L2 cells transformed with a vector encoding Cdn-1 as described in Example 4 were
35 grown in RPMI supplemented with 10% fetal bovine serum

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(FBS) for the anti-fas experiment or 0.1% FBS for serum deprivation experiments. In the case of the anti-fas experiment, after washing with fresh medium, the cells were suspended in RPMI supplemented with 10% FBS, exposed to anti-fas antibodies and the kinetics of cell death in response to an apoptosis inducing agent were analyzed by flow cytometry with FACScan. In the case of the serum deprivation experiment, the WI-L2 cells were resuspended in RPMI supplemented with 0.1% FBS and apoptosis was monitored according to the method described by Henderson et al. (1993) Proc. Natl. Acad. Sci. USA 90:8479-8483. Other methods of inducing apoptosis include, but are not limited to, oxygen deprivation in primary cardiac myocytes, NGF withdrawal, glutathione depletion in the neural cell line GTI-7 or TNF addition to the HT29 cell line. Apoptosis was assessed by measuring cell shrinkage and permeability to propidium iodide (PI) during their death. In addition, any other method of assessing apoptotic cell death may be used.

Figure 9 shows the anti-apoptotic response of various WI-L2 transformants to anti-Fas treatment. Figure 8 shows the anti-apoptotic response of various WI-L2 transformants to serum deprivation. In Figure 9, duplicate wells containing 3×10^5 cells were incubated with 50 ng/ml of the cytotoxic anti-Fas antibody for 24 hours. Cell death was then analyzed by flow cytometry with FACScan. The proteins expressed from each construct are shown beneath the columns. Since many of the constructs are truncation or deletion variants, the exact amino acids expressed are also indicated. As can be seen, all of the transformants had some protective effect when compared to the control transformant containing the pREP7 vector alone. The most apoptosis-resistant transformant was the *Cdn-1A2* expressing cell line, in which over 90% of the cells survived anti-fas treatment. Significant protection was also observed in transformants expressing

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full length *Cdn-1* (1-211) and *Cdn-1Δ1*, followed by *Bcl-2A* and *Bcl-2* expressing cell lines.

Cdn-1Δ1 and *Cdn-1Δ2* are lacking the nucleotides encoding the N-terminal 59 and 70 amino acids, respectively, of full length *Cdn-1*. The observation that expression of *Cdn-1Δ2* is more effective at blocking apoptosis than full length *Cdn-1* suggests that smaller, truncated *Cdn-1* molecules may be potent therapeutics.

Example 6

10 Determination of other *Cdn* genes and Cloning of the *Cdn-2* Gene

Southern blot analyses of human genome DNA and a panel of human/rodent somatic cell DNAs indicated that at least 3 *Cdn* related genes and that they resided in
15 chromosomes 6, 11 and 20. PCR/sequence analysis of the three hybrid DNAs showed that *Cdn-1* was on chromosome 6 and that two closely related sequences were on chromosome 20 (designated *Cdn-2*) and chromosome 11 (designated *Cdn-3*). We have cloned the *Cdn-2* and *Cdn-3* genes and
20 sequenced them. Interestingly, both *Cdn-2* and *Cdn-3* do not contain introns and have all of the features of processed genes that have returned to the genome. *Cdn-3* has a nucleotide deletion, causing a frame shift and early termination and thus is probably a pseudogene.
25 Both, however, have promoter elements [CCAAT, TATAAA boxes] but are probably not transcribed as determined by Northern blot analyses with *Cdn-2* and *Cdn-3* specified probes.

900,000 clones from a human placenta genomic library
30 in the cosmid vector pWE15 (Stratagene, La Jolla, CA) were screened with a 950 bp *BglIII-HindIII* cDNA probe containing the entire coding region of *Cdn-1*. The probe was ³²P-labeled according to the method of Feinberg and Vogelstein (1984) Anal. Biochem. 137:266-267. The
35 library was processed and screened under high stringency hybridization and washing conditions as described by

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Sambrook et al. (1989) Molecular Cloning, 2nd edition, Cold Spring Harbor Laboratory Press. Ten double positive clones were further purified by replating and screening as above. Plasmid DNA was purified using the Wizard
5 Maxiprep DNA Purification System as described by the supplier (Promega Corp., Madison, WI) and analyzed by *EcoRI* restriction enzyme mapping and Southern blotting. The probe used for Southern blotting and hybridization conditions was the same as above.

10 The cosmid clones fell into two groups as judged by *EcoRI* restriction analysis and Southern blotting. Cosmid clones (*cos*) 1-4 and 7 displayed one distinct pattern of *EcoRI* generated DNA fragments and contained a single 6.5 kb hybridizing *EcoRI* DNA fragment. *Cos2* and *Cos9* fell
15 into the second group that was characterized by a 5.5 kb hybridizing *EcoRI* DNA fragment. The 6.5 kb DNA fragment from *cos2* and the 5.5 kb DNA fragment from *cos9* were subcloned into pBluescript SK⁻ (Stratagene, La Jolla, CA) using standard molecular biological techniques (Sambrook
20 et al. as above). Plasmid DNA was isolated and the DNA inserts from two subclones, A4 (from *cos2*) and C5 (from *cos9*) were mapped with *BamHI*, *HindIII* and *EcoRI* and analyzed by Southern blotting as described above. Smaller restriction fragments from both clones were
25 subcloned into M13 sequencing vectors and the DNA sequence was determined.

The sequence of A4 contains an open reading frame that displays 97% amino acid sequence identity with *Cdn-1*. (Figure 5) The high degree of sequence identity
30 of this gene with *Cdn-1* indicates that it is a new *Cdn-1* related gene and therefore will be called *Cdn-2*. A sequence comparison of the encoded *Cdn-2* protein and the other members of the *Bcl-2* family is shown in Figure 6. *Cdn-2* contains the conserved regions, BH1 and BH2, that
35 are hallmarks of the *Bcl-2* family, and displays a lower overall sequence identity (~20-30%) to other members, which is also characteristic of the *Bcl-2* family. *Cdn-3*

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has a frame shift resulting in a shorter, unrelated polypeptide and therefore does not contain the structural features of *Cdn-1*, *Cdn-2* or other *Bcl-2* family members.

Example 7

5 Chromosomal Localization of the *Cdn-1*, *Cdn-2* and *Cdn-3* Genes

Southern blot analysis of a panel of human/rodent somatic cell hybrid DNAs (Panel #2 DNA from the NIGMS, Camden, NJ) and fluorescent in situ hybridization (FISH) 10 of metaphase chromosomes were used to map the *Cdn* genes to human chromosomes. For Southern blotting, 5 µg of hybrid panel DNA was digested with *EcoRI* or *BamHI/HindIII*, fractionated on 0.8% or 1% agarose gels, transferred to nitrocellulose and hybridized with the 15 *Cdn-1* probe. Hybridization and washing conditions were as described above. For FISH, the *Cdn-2* subclone, A4, was biotinylated using the Bionick Labeling System (Gibco BRL, Gaithersburg, MD) and hybridized to metaphase chromosomes from normal human fibroblasts according to 20 the method described by Viegas-Pequignot in *In Situ Hybridization, A Practical Approach*, 1992, ed. D.G. Wilkinson, pp. 137-158, IRL Press, Oxford. Probe detection using FITC-conjugated avidin and biotinylated goat anti-avidin was according to the method described by 25 Pinkel et al. (1988) Proc. Natl. Acad. Sci. USA 85:9138-9142.

Southern blot analysis showed three hybridizing *EcoRI* bands in the human DNA control that were approximately 12 kb, 11 kb and 5.5 kb in length. 30 Analysis of the somatic cell hybrid DNA indicated that the 12 kb band was in two different samples, NA10629, which contained only human chromosome 6, and NA07299, which contained both human chromosomes 1 and X and, importantly, a portion of chromosome 6 telomeric to p21. 35 The 11 kb band was in NA13140, which contains human chromosome 20. The 5.5 kb hybridizing band was found

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only in sample NA10927A, which contained human chromosome 11. PCR/DNA sequencing analysis of these hybrid DNA samples using primers for *Cdn-1*, *Cdn-2* or *Cdn-3* showed *Cdn-1* sequences in NA10629 (the chromosome 6-containing hybrid DNA) and NA07299 (the chromosome 1, X and 6pter >p21-containing hybrid DNA), indicating that the *Cdn-1* gene resides on chromosome 6, telomeric to p21. *Cdn-2* sequences were found in NA13140, indicating the *Cdn-2* gene resides on chromosome 20, and *Cdn-3* sequences were found in NA10927A, indicating the *Cdn-3* gene resides on chromosome 11.

Example 8

Modulation of apoptosis by *Cdn-1* and *Cdn-2* in FL5.12 cells

FL5.12 is an IL-3-dependent lymphoid progenitor cell line (McKearn et al. (1985) Proc. Natl. Acad. Sci USA 82:7414-7418) that has been shown to undergo apoptosis following withdrawal of IL-3 but is protected from cell death by overexpression of *Bcl-2*. Nunez et al. (1990) J. Immunol. 144:3602-3610; and Hockenbery et al. (1990) Nature 348:334-336. To assess the ability of *Cdn-1* and *Cdn-2* to modulate apoptosis, cDNAs encoding *Cdn-1*, *Cdn-2*, two truncated forms of *Cdn-1* (described below) and *Bcl-2* were ligated into the mammalian expression vector, pcDNA3 (Invitrogen, San Diego, CA) and stably introduced into the mouse progenitor B lymphocyte cell line FL5.12 by electroporation and selection in media containing the antibiotic G418. Assays were then performed on bulk transformants as described below.

The effects of the overexpressed genes on FL5.12 cell viability were examined at various times following withdrawal of IL-3 and are shown in Figure 10. Cell viability was assessed by propidium iodide (PI) exclusion on a flow cytometer (Becton Dickinson FACScan). *Bcl-2* expression protected the cells significantly from cell death while *Cdn-1* appeared to enhance cell death when

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compared to the vector control. *Cdn-2* expression conferred a low level of protection from cell death at earlier times but was insignificant at later time points. Interestingly, *Cdn-1Δ2* gave a moderate level of protection against cell death. *Cdn-1-112*, a molecule that contains the N-terminal 112 amino acids of *Cdn-1*, also appeared to partially protect the FL5.12 cells although at lower levels than *Bcl-2*.

As shown in Example 7, expression of *Cdn-1* and *Cdn-1Δ2* in WI-L2 cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis and serum withdrawal. Taken together, these data suggest that the various *Cdn* molecules are capable of modulating apoptosis in a positive or negative manner, depending on the cell type and apoptotic stimuli. Thus, they are effective in preventing cell death such as in the post-ischemic reperfusion tissue damage in the heart or in inducing cell death in cells that have escaped apoptotic control, as is the case in various cancers.

Example 9

IFN- γ induces *Cdn-1* mRNA expression in HT-29 cells

It has been shown that the human colon carcinoma cell line HT-29 is sensitive to the cytotoxic effect of anti-Fas antibody or TNF only after treatment with IFN- γ . Yonehara et al. (1989) J. Exp. Med. 169: 1747-1756. These IFN- γ treated cells also show enhanced apoptosis following serum deviation or cycloheximide treatment. This induced sensitivity of HT-29 cells to apoptotic stimuli may be partly due to the concomitant upregulation of the TNF receptor and Fas antigen that is seen following IFN- γ treatment. Yonehara et al. (1989). However, the increased cell death seen following serum deprivation or cycloheximide treatment suggests that other apoptotic mechanisms may be induced by IFN- γ . Modulation of the levels of *Bcl-2* family members by IFN- γ is another possible mechanism for the induced

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sensitivity of HT-29 cells to apoptotic stimuli. An increase in *Cdn-1*, *Bax* or *Bcl-x_s* expression and/or a decrease in *Bcl-2* or *Bcl-x_L* expression could result in enhanced sensitivity of the cells to cytotoxic agents.

- 5 To test this possibility, the mRNA levels of *Bcl-2* family members in untreated and IFN- γ treated HT-29 cells were examined by Northern blot analysis using the methods and conditions described in Example 2. *Cdn-1* mRNA levels were increased approximately 10X following IFN- γ
- 10 induction whereas *Bax* and *Bcl-x* mRNA levels remained unchanged. *Bcl-2* mRNA was below detectable levels in both untreated and IFN- γ treated cells. It remained possible that the ratio of *Bcl-x_s* to *Bcl-x_L* transcripts could have increased upon IFN- γ treatment but would not
- 15 be detected by Northern blot analysis due to the small difference in size between the transcripts. This was the case with unstimulated versus PMA plus ionomycin stimulated thymocytes as determined by Boise et al. (1993) Cell 74:597-608. Using semiquantitative PCR, they
- 20 showed that the ratio of *Bcl-x_s* to *Bcl-x_L* increased following stimulation. Using similar PCR techniques it was demonstrated that the ratio of *Bcl-x_s* to *Bcl-x_L* mRNA remained unchanged following IFN- γ treatment of HT-29 cells and that the predominant transcript was *Bcl-x_L*
- 25 (>90%).

- Thus there is a positive correlation between the upregulation of *Cdn-1* transcripts and the HT-29 tumor cells line following IFN- γ treatment and increased susceptibility to cell death. These results indicate
- 30 that there are positive modulators of *Cdn-1* in tumor cells and that they may be useful in treating some tumors when co-administered with appropriate apoptosis inducing agents.

- Although the foregoing invention has been described
- 35 in some detail by way of illustration and example for purposes of clarity of understanding, it will be apparent to those skilled in the art that certain changes and

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modifications may be practiced. Therefore, the description and examples should not be construed as limiting the scope of the invention, which is delineated by the appended claims.

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We claim:

1. A composition comprising a substantially purified nucleotide sequence encoding a *Cdn*.
2. The composition according to claim 1
5 wherein the nucleotide sequence is derived from genomic DNA.
3. The composition according to claim 1 wherein the *Cdn* is *Cdn-1*.
4. The composition according to claim 3
10 having the nucleotide sequence depicted in Figure 3.
5. The composition according to claim 1 wherein the *Cdn* is *Cdn-2*.
6. The composition according to claim 5 having the nucleotide sequence depicted in Figure 5.
- 15 7. A composition comprising a recombinant DNA vector encoding a *Cdn*.
8. The composition according to claim 7 wherein the *Cdn* is *Cdn-1*.
9. The composition according to claim 8
20 wherein the nucleotide sequence is depicted in Figure 3.
10. The composition according to claim 7 wherein the *Cdn* is *Cdn-2*.
11. The composition according to claim 10 wherein the nucleotide sequence is depicted in Figure 5.

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12. The recombinant DNA vector according to claim 7 wherein expression of the sequence encoding the *Cdn* under control of an inducible promoter.

13. A composition comprising a cell
5 transfected with a recombinant DNA vector encoding a *Cdn*.

14. The composition according to claim 13 wherein the *Cdn* is *Cdn*-1.

15. The composition according to claim 14 wherein the nucleotide sequence is depicted in Figure 3.

16. The composition according to claim 13
10 wherein the *Cdn* is *Cdn*-2.

17. The composition according to claim 16 wherein the nucleotide sequence is depicted in Figure 5.

18. A transgenic animal comprising a
15 recombinant DNA vector encoding a *Cdn*.

19. The transgenic animal according to claim 18 wherein the *Cdn* is *Cdn*-1.

20. The transgenic animal according to claim 19 wherein the *Cdn* nucleotide sequence is depicted in
20 Figure 3.

21. The transgenic animal according to claim 18 wherein the *Cdn* is *Cdn*-2.

22. The transgenic animal according to claim 21 wherein the *Cdn* nucleotide sequence is depicted in
25 Figure 5.

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23. A composition comprising a substantially purified Cdn protein.

24. The composition according to claim 23 wherein the protein is Cdn-1.

5 25. The composition according to claim 24 wherein the nucleotide sequence is depicted in Figure 3.

26. The composition according to claim 23 wherein the Cdn is Cdn-2.

10 27. The composition according to claim 26 wherein the nucleotide sequence is depicted in Figure 5.

28. The composition according to claim 23 wherein the proteins are expressed by recombinant DNA.

29. The composition according to claim 23 wherein the proteins are native proteins.

15 30. A composition comprising the proteins according to claim 23 and a pharmaceutically acceptable buffer.

20 31. The composition according to claim 30 wherein the proteins are present in therapeutically effective amounts.

32. A composition comprising a monoclonal or polyclonal antibody which recognizes a Cdn but is substantially unreactive with other members of the Bcl family.

25 33. A method of detecting the presence of a Cdn protein in a biological sample comprising the steps of:

a) obtaining a cell sample;

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b) lysing or permeabilizing the cells to antibodies;

c) adding anti-*Cdns*-specific antibodies to the cell sample;

5 d) maintaining the cell sample under conditions that allow the antibodies to complex with the *cdn*; and

e) detecting the antibody-*cdn* complexes formed.

10 34. The method according to claim 33 wherein the *Cdn* is *Cdn*-1.

35. The method according to claim 34 wherein the nucleotide sequence is depicted in Figure 3.

15 36. The method according to claim 33 wherein the *Cdn* is *Cdn*-2.

37. The method according to claim 36 wherein the nucleotide sequence is depicted in Figure 5.

38. The method according to claim 32 wherein the cell sample comprises T cells.

20 39. A method for detecting the expression of a *Cdn* gene in a biological sample comprising the steps of identifying the presence of RNA encoding the *cdn*.

40. The method according to claim 39 wherein the method for identifying the *Cdn*-1 or *Cdn*-2 mRNA is
25 Northern blotting.

41. A method identifying *Cdn* mRNA comprising the steps of:

a) obtaining a cell sample;

b) obtaining RNA from the cell sample;

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c) performing a polymerase chain reaction on the RNA using primers corresponding to unique regions of the *Cdn*; and

d) detecting the presence of products of the polymerase chain reaction.

42. A method of modulating apoptosis-induced cell death comprising modulating the endogenous levels of a *Cdn*.

43. The method according to claim 40 wherein the *Cdn* is *Cdn*-1.

44. The method according to claim 43 wherein the nucleotide sequence is depicted in Figure 3.

45. The method according to claim 42 wherein the *Cdn* is *Cdn*-2.

46. The method according to claim 45 wherein the nucleotide sequence is depicted in Figure 5.

47. The method according to claim 41 wherein the *Cdn* is increased by modulating expression of an endogenous *cdn* gene.

48. The method according to claim 46 wherein the *Cdn* gene expressed is encoded by a recombinant gene.

49. The method according to claim 48 wherein expression of the gene is under the control of an inducible promoter.

50. The method according to claim 49 wherein the cells and transfected *ex vivo* and further comprising the steps of reintroducing the transfected cells into the animal.

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51. The method according to claim 50 wherein the cells are T lymphocytes.

52. The method according to claim 49 wherein the recombinant gene is transfected into cells *in vivo*.

5 53. A method of treating apoptosis in a patient in need thereof comprising administering a therapeutically effective amount of Cdn.

54. The method according to claim 53 wherein the Cdn is Cdn-1.

10 55. The method according to claim 54 wherein the nucleotide sequence is depicted in Figure 3.

56. The method according to claim 53 wherein the Cdn is Cdn-2.

15 57. The method according to claim 56 wherein the nucleotide sequence is depicted in Figure 5.

58. The method according to claim 53 wherein the Cdn is administered for any indication for which superoxide dismutase has been indicated.

20 59. A method of assaying for interactions between Cdns and proteins which bind specifically to Cdns comprising the steps of contacting purified Cdn with cell lysates containing a protein which may bind to the Cdn under conditions which allow binding of the protein and the Cdn;

25 isolating the Cdn;
contacting the isolated Cdn with a binding partner specific for the protein under conditions which allow binding of the binding partner and the Cdn; and

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measuring the amount of binding partner bound to the protein.

60. The method according to claim 59 wherein the cell lysate is a yeast lysate.

5 61. The method according to claim 59 wherein the binding partner is an antibody.

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5'- AGATCTGAATTC AA(C/T) TGG GGI (C/A)GI (A/G)TX GTX GC -3'

Bclx 1-32

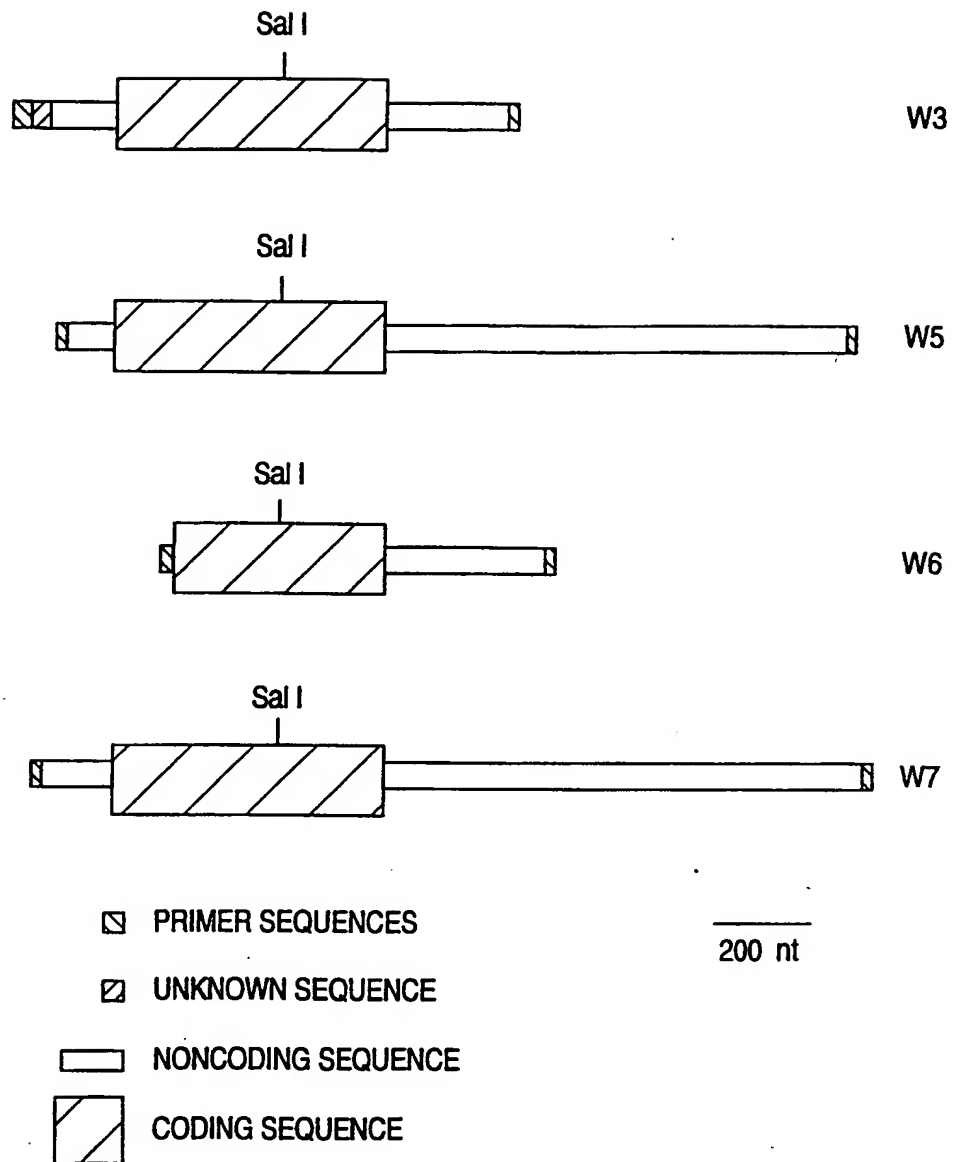
5'- AGATCTAAGCTT GTC CCA ICC ICC XTG XTC (C/T)TG (A/T/G)AT CCA -3'

Bclx 2-39

FIG. 1

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**FIG. 2**

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>Aha2

80

GGACAAGTAA AGGCTACATC CAGATGCCGG GAATGCACTG ACGCCCATTC CTGGAAACTG GGCTCCCACT CAGCCCCTGG

>Sma1 >BamH1

160

GAGCAGCAGC CGCCAGCCCC TCGGACCTCC ATCTCCACCC TGCTGAGCCA CCCGGGTTGG GCCAGGATCC CGGCAGGCTG

ATCCCGTCCT CCACTGAGAC CTGAAAA ATG GCT TCG GGG CAA GGC CCA GGT CCT CCC AGG CAG GAG TGC

M A S G Q G P G P P R Q E C>

240

GGA GAG CCT GCC CTG CCC TCT GCT TCT GAG GAG CAG GTA GCC CAG GAC ACA GAG GAG GTT TTC CGC

G E P A L P S A S E E Q V A Q D T E E V F R>

320

AGC TAC GTT TTT TAC CGC CAT CAG CAG GAA CAG GAG GCT GAA GGG GTG GCT GCC CCT GCC GAC CCA

S Y V F Y R H Q Q E Q E A E G V A A P A D P>

>Nco1

400

GAG ATG GTC ACC TTA CCT CTG CAA CCT AGC AGC ACC ATG GGG CAG GTG GGA CGG CAG CTC GCC ATC

E M V T L P L Q P S S T M G Q V G R Q L A I>

480

>Pst1

ATC GGG GAC GAC ATC AAC CGA CGC TAT GAC TCA GAG TTC CAG ACC ATG TTG CAG CAC CTG CAG CCC

I G D D I N R R Y D S E F Q T M L Q H L Q P>

>Sca1_

560

ACG GCA GAG AAT GCC TAT GAG TAC TTC ACC AAG ATT GCC ACC AGC CTG TTT GAG AGT GGC ATC AAT

T A E N A Y E Y F T K I A T S L F E S G I N>

TGG GGC CGT GTG GTG GCT CTT CTG GGC TTC GGC TAC CGT CTG GCC CTA CAC GTC TAC CAG CAT GGC

W G R V V A L L G F G Y R L A L H V Y Q H G>

FIG. 3A SUBSTITUTE SHEET (RULE 26)

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>Sal1

640

CTG ACT GGC TTC CTA GGC CAG GTG ACC CGC TTC GTG GTC GAC TTC ATG CTG CAT CAC TGC ATT GCC
L T G F L G Q V T R F V V D F M L H H C I A>

720

CGG TGG ATT GCA CAG AGG GGT GGC TGG GTG GCA GCC CTG AAC TTG GGC AAT GGT CCC ATC CTG AAC
R W I A Q R G G W V A A L N L G N G P I L N>

800

GTG CTG GTG GTT CTG GGT GTG GTT CTG TTG GGC CAG TTT GTG GTA CGA AGA TTC TTC AAA TCA TGA
V L V V L G V V L L G Q F V V R R F F K S >

>Afl2

880

CTCCCAA GGGTCCCCTT TGGGTCCCGG TTCAGACCCC TGCCTGGACT TAAGCGAAGT CTTTGCCTTC TCTGTTCCCT

>Hind3

960

TGCAGGGTCC CCCCTCAAGA GTACAGAAGC TTTAGCAAGT GTGCACTCCA GCTTCGGAGG CCCTGCGTGG GGGCCAGTCA

>Pst1

>Apa1

1040

GGCTGCAGAG GCACCTCAAC ATTGCATGGT GCTAGTGCCC TCTCTCTGGG CCCAGGGCTG TGCCCGTCTC CTCCTCAGC

1120

TCTCTGGGAC CTCCTTAGCC CTGTCTGCTA GGCCTGGGG AGACTGATAA CTTGGGGAGG CAAGAGACTG GGAGCCACTT

1200

CTCCCCAGAA AGTGTTTAAC GGTTTTAGCT TTTTATAATA CCCTTGTGAG AGCCCATTC CACCATTCTA CCTGAGGCCA

>Aha2

1280

GGACGTCTGG GGTGTGGGA TTGGTGGGC TATGTTCCCC AGGATTGAGC TATTCTGGAA GATCAGCACC CTAAGAGATG

1360

GGACTAGGAC CTGAGCCTGG TCCTGGCCGT CCCTAAGCAT GTGTCCGAGG AGCAGGACCT ACTAGGAGAG GGGGGCCAAG

FIG. 3B

SUBSTITUTE SHEET (RULE 26)

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1440
* * * * *
GTCCTGCTCA ACTCTACCCC TGCTCCCAATT CCTCCCTCCG GCCATACTGC CTTTGCAGTT GGACTCTCAG GGATTCTGGG

1520
* * * * *
CTTGGGGTGT GGGGTGGGGT GGAGTCGCAG ACCAGAGCTG TCTGAACTCA CGTGTCAAGG GCCTCCAAGC CTGCCTCCCA

1600
* * * * *
AGGTCCTCTC AGTTCTCTCC CTTCCTCTCT CTTATAGAC ACTTGCTCCC AACCCATTCA CTACAGGTGA AGGCTCTCAC

1680
* * * * *
CCATCCCTGG GGGCCTTGGG TGAGTGGCCT GCTAAGGCTC CTCCTTGCCC AGACTACAGG GCTTAGGACT TGGTTTGTTA

1760
* * * * *
TATCAGGGAA AAGGAGTAGG GAGTTCATCT GGAGGGTCT AAGTGGGAGA AGGACTATCA ACACCACTAG GAATCCCAAG

>BamH1
|
1840
* * * * *
GGTGGATCCT CCCTCATGGC TCTGGCACAG TGTAATCCAG GGGTGTAGAT GGGGGAAGTG TGAATACTTG AACTCTGTTT

1920
* * * * *
CCCCACCCTC CATGCTCCTC ACCTGTCTAG GTCTCCTCAG GGTGGGGGGT GACAGTGCCT TCTCTATTGG CACAGCCTAG

2000
* * * * *
GGTCTTGGGG GTCAGGGGGG AGAAGTTCTT GATTGAGCCA AATGCAGGGA GGGGAGGCAG ATGGAGCCCA TAGGCCACCC

* * * * *
CCTATCCTCT GAGTGTGTTG AAATAAACTG TGCAATCCCC TCAAAAAAAAA AA

FIG. 3C

SUBSTITUTE SHEET (RULE 26)

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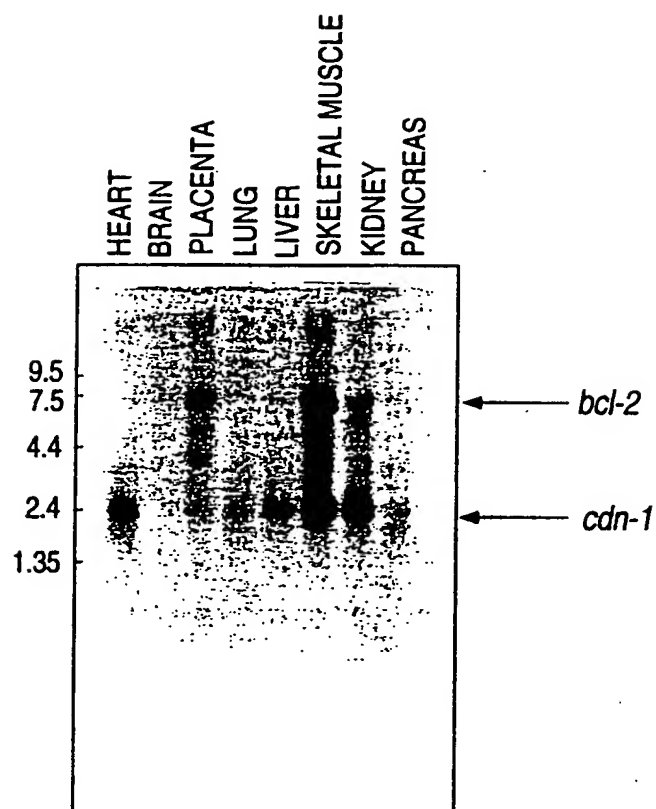


FIG. 4

```

>EcoRI
|
* * * * *
GAATTCCTGG CCGCAATTAA CCCTCACTAA AGGATCCTC CTGCCTTGGT CTCCCAAAAT GTTGAGATTA TAGGCATGAG
80
* * * * *
CCCACCACGC CTGGCTGGGG TTTTGTTTTT GTTTTTTTAA CATTTGTCAC ATTTACAAAA GGTATTTTCT AATCTCTGAG
160
* * * * *
AAAAGTGCTA TAATGTCTAA TGATACTTTA TATTGGACA GCACTTTCGT TTGTTTTTTT TGGCGGGGGG GGTGGGAGAA
240
* * * * *
GTCAAGTAAC TTACATATAG TGAAATTTAC CCTTCTTGAG TATGCAGTTC AGTGAGTTTT GATAAATGTG TAATGGTAGT
320
* * * * *
GTAATCACTA CCACAGTCAA GACATGGACA ATTTTCATTA CCCCACGAAG GTCCCTCATG TGTGGTTAGA GTCAGCCCTC
400
* * * * *
CCATCAGCAC AGTCTGGCA GCCACTGACC TGCTTCTGT CCTACTGTT TTGCTTTTC CAGAATGTCA TTTAAGTGAC
480
* * * * *
ATCATTCAAT ATGGAGACTT GTTTTATTTT TTATTTTITA TTTTGTGAGA AGGAGTCTCG CTCTGTTGC CCAGGCTAGA
560
* * * * *
>EcoRI
|
* * * * *
GTGCAATGCT GTGATTTCGG CTCAGTCAA CCTCCGCTC CCGGGTTCAA GTGATTCTCC TGCCTCAGCC TCCCGAGTAG
640
* * * * *
TTCGGGACCA CAGGCGTACA CCACCATGCC CAGCTAATTT TTTTTTTTTT TGAGATGGAG TCTCGCCCTG TCACCCAGGC
720
* * * * *
>EcoRI
|
* * * * *
TAGAGTCCAG TGGCATGATC TGCCTCACT GCCAAGCTCC TGCCTCCCGG GTTTCAGGCC ATTCCTCTGC CTCAGCTCC
800
* * * * *
>EcoRI
|
* * * * *
CGAGTATGCC CCGCTAATTT TTGATTTTTT AGTAGAGACG GGGTTTCCCC ATGTGGCCA GGCTAGTCTC AAACCTCTGA
880
* * * * *

```

RECTIFIED SHEET (RULE 91)

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960
* * * * *
CCTCAAGTAA TCCGCTGCC TTGGCTCCA AAGTCTGGG ATTACAGGTG TGAGCCACCG CGCCCAGCCC ATTATGTAGC

>SpeI
|
1040
* * * * *
TTTTGTGCC CCACTTCTCC CACTTAGCAT AATGCTTTT GAGATTCATC TGTATTACTA GTGCATCTGT AGTTCTTTCC

1120
* * * * *
TTTTATGCC TTGGGTGTT TTTTGTITT GTTTTGTIT TTGAGATAGG GTCTCACTCT GTTGCCAGG GTGGAGTGA

>EcoR5
|
1200
* * * * *
CTATCGCAGC TCTCCGAAC CTCCACCTCC CAGGCTCAAG ATATCCTCCC ACCTCAGCCT CCTGAGTAGC TGGAAATACA

>NcoI
|
1280
* * * * *
AGTGTGTGTG CCACCATGCC GGTAAATTT TTTTCTTTT TTTTTTTTT TTTTCAATT TTGTGGAAG CACCATGGAG

>BclI
|
>SphI
|
1360
* * * * *
CCGCCTGAGC CTGGCTGAGC CTAAAAGCCC TGTGGTGCAT GCCTGGCCAA TTTTGTATT TTTTAGTAGA GACGGGATT

1440
* * * * *
TGCCATGTCG CCCAGGCTGG TCTGGAATC CTGGTCTCAG GTGATTCTCC TGCTTCGGCC TCCCAAGTAG CTGGGGTTAC

1520
* * * * *
AGGCATGTGC CACCATGCTC AGCCCTCCCG TCAGCACAGT CCTGGCAGCC ACTGGCCTGG TTTCTGTCCC TACTGTTTTG

1600
* * * * *
CCTTTTACTG GTCTCCATGC TCACCTAAAT TTTTTTTAT TTTTGTAGA GACAGATTCT CGCAATGTTG CTCAGGCTAG

1680
* * * * *
TCTGAACTC CCGGCTTCAA GCAATCCTCC CACCTCAGTC CTCAAAGTT CTGGAATTAC AGGCATGAAT CACTGTGCCA

FIG. 5B

RECTIFIED SHEET (RULE 91)

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>Aha3
|
>Dra1
|

1760

* * * * *

GTGTTGCATT CCAAAGCATG GATACATCAC AGTTTTTAAA ATGTTTACCA ATGTAAATGG CCCGTTTTAA TATGAGAATA

1840

* * * * *

ACTAATGTTG AAGAGAGTGC TACAAAGAGG ATCATGGTCG TGATGTGTAG ACACAAAAAT GAGGTTAGAA GACAGTAAGG

1920

* * * * *

TGAGGGCCGG GCACAGTGGC TCATGCTTGT AATCCTAGCA CTTTGGGAGG TGCAGGTGGG AGGATTGCTT GAGGCCAGGA

2000

* * * * *

GCTGGAGACA AGTCCAGGCA ACACAGCGAG TCCCTGCCTT TATAAAAAAT CAGAAATTAA AAAAGCCTTG GCGGTGGCTC

>Bcl1
| 2080

* * * * *

ACGCCTGTAA TCCCAGCACT TTGGGAGGCC GAGACGGGTG GATCACGAAG TCAGGAGTTC AAGACCAGCT TGGCCAAGAT

2160

* * * * *

GGTGAACCC TGTCTCTACT AAAAATAAAA AAAAAAATT AGCCAGTCGT GGTGGTGGCA CCTGTAATCC CAGCTACTCA

2240

* * * * *

GGAGGCTGAG GCAGGAGAAT CGCTTGAACC CAGGAGGCGG AGTTTGCAGT AAGCCAAGGT GCGCCACTGC ACTCCAGCCT

2320

* * * * *

GGGCAACAGA GTAAGACTCT GTCTCAAAAA AAAACAAAA ACAAAAAAAC AAAAAAACA CAGGCCGGCG CAGTGGCTCA

>Sca1
| 2400

* * * * *

TGCCTATAAT CCAAGTACTT TGGGAGGCCA AGGCAGGCGG ATCGCAAAGT CAGGAGTTCG AGACCAGCCT GGCCAATATG

2480

* * * * *

GTGAAACCCT GTTCTGCTA AAAATACAAA AAATAGCCAG GTGTGGTGGG AAGCGCCTGT AGTCCAGCT ACTCAGGAGG

>Sma1
| 2560

* * * * *

CTGAGGCAGG AGAATCGCTT GAACCCGGGA GGCAGAAGTT GCAGTGAGCT GAGATTGCGC CACTGCACTC CAGCCTGGGC

FIG. 5C

RECTIFIED SHEET (RULE 91)

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```

                                >Aha3
                                |
                                >Dra1
                                |
*      *      *      *      *      *      *      *      2640
AACAGAGCGA GACTCCATCT CAAAGAAAA AAAGCCAAAA CATAGTAAGG TGAGGGTGAA ACTTCTCTTT TAAAAAATG

*      *      *      *      *      *      *      *      2720
TTTACATAGA AACAACTAA ATGGACAAAA TGGATATAAA CAAAAATGTT ATCGGTGGTT ATTTTGGGC AGTAGAATTA

*      *      *      *      *      *      *      *      2800
TAGGTTTTTA ATTTCTTTTG CTTATTTATA GTTCAAAAA TTTCAATTT TAATATAAAT TAATGTGCTC TATTATAGA

*      *      *      *      *      *      *      *      2880
GACAATACAT GAAATATACT TAATAAAAA TCAAATGTTA TAGAACTGAA AAAGATGAAA AGTAAAAACA ACCTATTCCC

*      *      *      *      *      *      *      *      2960
CAGAGGTAGC CACTGTCCAT AGTTTCTATT TTAGATTCTT TCCTTTATAC AAGATTATTA TAGCTTCTAT TTTTGGTGT

*      *      *      *      *      *      *      *      3040
ATGAACTGTA GTCCTAGAGG ATTTTATTAG TTATGAGTTC TATAACTAAG ATCCATCATC TTAGTTGCTA AGAACGTAGA

>Dra1
|
>Aha3
|
*      *      *      *      *      *      *      *      3120
TACTGAGAAC ATCATTTAAA AAAACATTTT TGGCTGGCAC CTCTATGATC ACTGGAGTCT CGCGGGTCCC TCAGGCTGCA

*      *      *      *      *      *      *      *      3200
CAGGGACAAG TAAAGGCTAC ATCCAGATGC TGGGAATGCA CTGACGCCCA TTCCTGGAAA CTGGGCTCCC ACTCAGCCCC

*      *      *      *      *      *      *      *      3280
TGGGAGCAGC AGCCGCCAGC CCCTCGGGAC CTCCATCTCC ACCCTGCTGA GCCACCCGGG TTGGGCCAGG ATCCCGGCAG

*      *      *      *      *      *      *      *     
GCTGATCCCG TCCTCCACTG AGACCTGAAA A ATG GCT TCG GGG CAA GGC CCA GGT CCT CCC AGG CAG GAG
M   A   S   G   Q   G   P   G   P   P   R   Q   E>

```

FIG. 5D

RECTIFIED SHEET (RULE 91)

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3360
 * * * * *
 TGC GGA GAG CCT GCC CTG CCC TCT GCT TCT GAG GAG CAG GTA GCC CAG GAC ACA GAG GAG GTT TTC
 C G E P A L P S A S E E Q V A Q D T E E V F>

3440
 * * * * *
 CGC AGC TAC GTT TTT TAC CAC CAT CAG CAG GAA CAG GAG GCT GAA GGG GCG GCT GCC CCT GCC GAC
 R S Y V F Y H H Q Q E Q E A E G A A P A D>

>Nco1
 |
 3520
 * * * * *
 CCA GAG ATG GTC ACC TTA CCT CTG CAA CCT AGC AGC ACC ATG GGG CAG GTG GGA CGG CAG CTC GCC
 P E M V T L P L Q P S S T M G Q V G R Q L A>

>Pst1
 |
 3600
 * * * * *
 ATC ATT GGG GAC GAC ATC AAC CGA CGC TAT GAC TCA GAG TTC CAG ACC ATG TTG CAG CAC CTG CAG
 I I G D D I N R R Y D S E F Q T M L Q H L Q>

>Sca1
 |
 3680
 * * * * *
 CCC ACG GCA GAG AAT GCC TAT GAG TAC TTC ACC AAG ATT GCC TCC AGC CTG TTT GAG AGT GGC ATC
 P T A E N A Y E Y F T K I A S S L F E S G I>

AAT TGG GGC CGT GTG GTG GCT CTT CTG GGC TTC AGC TAC CGT CTG GCC CTA CAC ATC TAC CAG CGT
 N W G R V V A L L G F S Y R L A L H I Y Q R>

3760
 * * * * *
 GGC CTG ACT GGC TTC CTG GGC CAG GTG ACC CGC TTT GTG GTG GAC TTC ATG CTG CAT CAC TGC ATT
 G L T G F L G Q V T R F V V D F M L H H C I>

3840
 * * * * *
 GCC CGG TGG ATT GCA CAG AGG GGT GGC TGG GTG GCA GCC CTG AAC TTG GGC AAT GGT CCC ATC CTG
 A R W I A Q R G G W V A A L N L G N G P I L>

3920
 * * * * *
 AAC GTG CTG GTG GTT CTG GGT GTG GTT CTG TTG GGC CAG TTT GTG GTA CGA AGA TTC TTC AAA TCA
 N V L V V L G V V L L G Q F V V R R F F K S>

FIG. 5E

RECTIFIED SHEET (RULE 91)

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```

                                >Af12
                                |
                                4000
*      *      *      *      *      *
TGA CTC CCAAGGGTGC CCTTTGGGGT CCCAGTTCAG ACCCCTGCCT GGACTTAAGC GAAGTCTTTG CCTTCTCTGC
*)

                                >Hind3
                                |
                                4080
*      *      *      *      *      *
TCCTTGCAGG GGTCCCCCT CAAGAGTACA GAAGCTTTAG CAAGTGTGCA CTCCAGCTTC GGAGGGCCCC TGTGTGGGGG

                                >Pst1
                                |
                                >Nco1
                                |
                                >Apa1
                                |
                                4160
*      *      *      *      *      *
CCAGTCAGGC TGCAGAGGCA CCTCAACATT CCATGGTGCT AGTGGGCCCT CTCTCTGGGC CCAGGGGCTG TGGCGTCTCC

                                >Apa1
                                |
                                >Aha2
                                |
                                4240
*      *      *      *      *      *
TCCCTCAGCT CTCTGGGACC TCCTTAGCCC TGTCTGCTAG GCGCTGGGGA GACTGATAAC TTGGGGAGGC AAGAGACTGG

                                4320
*      *      *      *      *      *
GAGCCACTTC TCCCAGAAA GTGTTTAATG GTTTAGCTT TTTATAATAC CCTTGTGAGA GCCCATTCAC ACCATTCTAC

                                >Aha2
                                |
                                4400
*      *      *      *      *      *
CTGAGGCCAG GACGTCTGGG GTGTGGGGAT TGGTGTGTCT ATGTTCCCCA GGATTCAGCT ATTCTGGAAG ATCAGCACCC

                                4480
*      *      *      *      *      *
TAAGAGATGG GACTAGGACC TGAGCCTGGT CCTGGCCGTC CCTAAGCATG TGTCCAGGA GCAGGACCTA CTAGGAGAGG

                                4560
*      *      *      *      *      *
GGGGCCAAGG TCCTGCTCAA CTCTACCCCT GCTCCCATTC CTCCTCCGG CCATACTGCC TTTGCAGTTG GACTCTCAGG

                                4640
*      *      *      *      *      *
GATTCTGGGC TTGGGGTGTG GGGTGGGGTG GAGTCGAGAC CAGAGCTGTC TGAAGTCATG TGCAGAAGC CCTCCAAGCC

                                4720
*      *      *      *      *      *
TGCTCCAG GGTCTCTCA GTTCTCTCC TTCTCTCTC CTTATAGACA CTTGCTCCA ACCCATTCAC TACAGGTGAA

```

FIG. 5F

RECTIFIED SHEET (RULE 91)

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>StuI

4800

* * * * *

GGCTCCTCAC CCCCATCCCT GGGCCTTGGG TGAGTAACCT GCTAAGGCCT CCTTGCCCAG ACTACAGGGC TTAGGACTTG

4880

* * * * *

GTTTGTATT TCAGGGAAAA GGAGTAGGGA GTTCATCTGG AGGGTTCTAA GTGGGAGAAG GACTATCAAC ACCACTAGGA

>BamH1

4960

* * * * *

ATCCAGAGG TGGGATCCTC CCTCATGGCT CTGGCACAGT GTAATCCAGG GGTGTAGATG GGGGAACGT GAATACTTGA

5040

* * * * *

ACTCTGTCC CCCACCCTCC ATGCTCCTCA CCTGTCTAGG TCTCCTCAGG GTGGGGGGTG AGAGTGCCTT CTCTATTGGG

5120

* * * * *

CACAGCCTAG GGTCTTGGGG GTCGGGGGGA GAAGTTCTTG ATTCAGCCAA ATGCAGGGAG GGGAGGCAGA TGGAGCCCAT

5200

* * * * *

AGGCCACCTC CTATCCTCTG AGTGTGGA AATAAAGTGT GCAATCCCCT CAAAAAATA AAAATAAAAA AAATAAAAAAT

5280

* * * * *

AAAAAACAT TTTTTCAG CAGGGAGTGG TGGTCCCAG CTGTAATCCC AGCACTTTGG GAGGCCAAGG CGTGCAATT

5360

* * * * *

GCTTCAGTTC AGGAGTTCAA GACCAGCTG GGAACATGG TGAAACCCCA TCTCTACTAA AAATAAAAAA TTAGCCAGGC

5440

* * * * *

ATAGTGTGCG GCACCTGTAC TCCAGCTAT TTGGGAGGCT GAGGTAGGAG AATTGCTTGA ACCCAGGAGG TGGAGGTTGC

5520

* * * * *

AGTGAGCTGA GATCAGGCCA CTGCACTCCA ACGTAGGTGA CAGAGATAGC CTCCTTCTAA AAAACAACC TTTTTCAG

>XbaI

5600

* * * * *

CCAAAACAAC TGAAGTTCCT CCCCACTGAC CACCTCAATT ATTTCTAGAT GCCTTGTTCG TGTCCAGACT GCGGTGATTC

5680

* * * * *

CCTGGGCTGA TCTGAGCCCG TGGCCTGAGT CATTGTCAGT TCCTCTAGCA GGTGGTCCCC CATGTCATGG CCCCTGTGAA

FIG. 5G

RECTIFIED SHEET (RULE 91)

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>Hind3
|

5760
* * * * *
ACCAGTTCCT TACCATCTCT GTTCATCGCT GCTCCCTAAG TTAGGCCCTG CATGTCTTGA GGGTAGGTTA GATTCAGAAA

5840
* * * * *
AGCTTTGGTC GCATCACTGC TTTCATAAAC TCAAATGAGA GGGAGGGAGG GAAGGCAGGA AGAAGGGAGG GAGTCCTTTC

5920
* * * * *
TCTCCACAG TGTGCATTAC CTCATGTAAC ACTTCTTGT AATGTGGTAG AATGTGTTG ACTTTGAATG AGACTTGGGT

6000
* * * * *
TTATTTTAT TTATTTATT ATTTATTTAT TTATTTATT TGAGATGGAG TTCACTCTT GTTGGCCAGG CTGGAGTGT

6080
* * * * *
GTGGCACGAT CTCTACTCAT TGCACCCTCC GCCTTCCAGG TTCAAACGAT TCTCCTGCCT CAGCCTCCCA AGTAGCTGGG

>Sph1
|

6160
* * * * *
ATTACAGGGG CATGCCACCA TGCCAGCTA ATTTTGTAT TTTTAGTAGG GACGGGGTT CACCATGTTG ACCAGGCTGG

6240
* * * * *
TCTGGAATC CTGATCTCAG GTGATCCACC TGCTCGGCC TCCCAAAGTG TTGGGATTAC AGGCGTGAGC CACCGTGCCT

6320
* * * * *
GGCCTGAGAC TTAAATCCAT CTCTTTTTT TCCTCTTTT TGAGACAGAG CCTCATTCTG TTCCCATG C TGAGTTTCA

>Bcl1
|

6400
* * * * *
TGGCGTGATT TTGGCTCACT GCAACCTTGG CCATCTGGGT TTGAGCAATT CTCGTGCCTC AGCCTCCTGA GTAGCTGGCA

6480
* * * * *
CTATAGTCAC ATGCCACCAC GCCCGGCTAA CTTTTTGT TTTTAGTAG AGACAGGGTT TCACTATGTT AGCCAGGCTG

>EcoR1
|

GTCTCGAATT C

FIG. 5H

cdn1	masgqgpgpprceqgepalpsaseeqvaadtveefrsyvrhqqeqeaeagvaapadpemt	
cdn2	masgqgpgpprceqgepalpsaseeqvaadtveefrsyvrhqqeqeaeagvaapadpemt	
bc12	mahagrtgyDNREIVMKYIHYKLSRGYEWdagdvgaapgaapaglfssqpghtphtaasrdpvarsp1qtpaapga	
bax	mdgsgeqprgggtsseqimktgalllqgfiqdragrmggeap	
bc1-x	msqSNRELVVDFLSYKLSQKGYSWsfdsveenteapegtesemetpsaingnpswhladspavngatghss	
mc1-1	...(+123 aa)eldgyepeplgrpavlp1lelvgesGmntstdgs1pstppaeeedeelyrqsleifisrylreqatgakdk	
A1	maeselmh1hslaehylqyvlq	
bhrf	maystreillalcirdsrvhngt1hvp1lelaar	
LMW5-HL	megeeliyhniineilvg	
ced9	mtrctadnsltnpayrrrtmatgemkeflgikgteptdfginsdaqdlpspsrqastrmsigesidgk1ndweepr1DIEGFVVDFYFTHRIRQNGMEWfgpg	
cdn1	1plqpsstmgQVGRQLAIIGDDINRRYDSEFOTMLQHLQPTAENAYEYFTKIATSLFESGI-NWGRVVALLGFGYRLALHVVYQHGLTGFLGOVTRFVDFMLHH	
cdn2	1plqpsstmgQVGRQLAIIGDDINRRYDSEFOTMLQHLQPTAENAYEYFTKIATSLFESGI-NWGRVVALLGFGYRLALHVIYQRLTGFLGOVTRFVDFMLHH	
bc12	agpalpvpvVHLTLRQAGDFFSRYYRDRFAEMSRQLH1tpftarqRFATVVEELFRDGV-NWGRIVAFEEFGGVMCVESVNREMSPLVDNIALWTEY-LNR	
bax	e1aldpvpqdaatk1seclkrigdeldsnmelqrmiaaytdtspreVFRVAADMFSDGNFNWGRVVALLFYFASKVLKALCTKVPELIRTIMGNTLDF-LRE	
bc1-x	darevipma-AVKQALREAGDEFELRYRRAFSDLTSQHLITPGTAVQSFQVWELFRDGV-NWGRIVAFESFGGALCVESVDKEMQVLSRIAANMATY-LND	
mc1-1	pmgrsgatsrka1ETLRVGGVQRNHETVFGMLRKLDTKNEDDVKLSRWMTVFSQVWELFRDGV-NWGRIVAFESFGGALCVESVDKEMQVLSRIAANMATY-LND	
A1	vpafesapsqacrv1qrva1svqakevkn1ksylddfhesidtar1f1NQVMEKEFEDGIINWGRIVITIFAGGVLKKLpgeqialdvca1kqvssfvaefi	
bhrf	etplrlspedtv1ryhvl1lee1ernsettetwnrf1tthetvhd1dfnsv1lei1fhD-LINWGRICGFIVFSARMAYCKDAN-HLESTVITAYNF-SEG	
LMW5-HL	ikyy1mndihelspyqqq1k11tyydeclnkqvt1fsltnaqe1ktQFTGVVTELFRgdps1gralawmawcmhact1ccnqstpyyvvdlsvrgmleam	
ced9	1pcgvqpehemrmvmgt1fekhaenfetfceeQ1lavpr1sfslyqdvrvrtvgnaqtdqcpHSYGRLLIGLISFGGFVAAKMMesve1qgqvrrn1fvyts1fIKT	
cdn1	CIAR--WIA-QR-GGWVAALNLGngpi1nv1vlgv1l1gqfvvrrfks	
cdn2	CIAR--WIA-QR-GGWVAALNLGngpi1nv1vlgv1l1gqfvvrrfks	
bc12	HLHT--WI--ODNGGWDFAVELYgpmpr1fdfsw1skt1ls1alvgacit1gay1ghk	
bax	RLLG--WI--ODQGGWDL1SYFgtptwtvt1fvagv1tas1tiwkkmg	
bc1-x	HLEP--WI--QENGWD1FVELYgnaaaesrkqerfnrwt1gmtvaggv1l1gslfsrk	
mc1-1	TKRD--WL1VKQ--RGWDGVEFFhved1eggirnv1la1fagvaggag1ay1lr	
A1	MNNTGEWI-RQ-NGGWEDg1fkkfepksgw1t1f1qmtqgiwem1f1lk	
bhrf	-LDG--WIHQ--GGWSt11edni1pgsr1rfswt1f1ag1t1sl1vicsyl1f1s1rgrh	
LMW5-HL	KHNL1P1WMISH--GGQEEFLAFslhsq1ysv1fn1ky1f1skf1cnh1f1rscvql1r1cn11	
ced9	-R1RN1WKE-H-NRSWDDFNT1Lgk1mqkedyeraeakvgrkrkqrrn1wsm1gagvtaga1g1vgvvvvcgrmmfslk	

SEQUENCE IDENTITY:

cdn1/cdn2 = 97%

FIG. 6

>EcoR1
|
* * * * *
GAATTCTGGT AATTAGTTAA ACAACCTTGA ACAAGTTGTT TCACCTTCTCT GAGTCTCAGT TTCTCACTCA AAAATGGTGA
* * * * *
160
ATAATTTGTA AGACTTCGCT AATAATCTAC GACTCTACAA GAGGCAATAG GGTACTGTGG ACAGAGAGCA GGCTTTGGAA
* * * * *
240
ACACACAAGA CTGGGTTTAG ATTCTGCAC TCCACCCAGT GTGTGACTTG GCCAAGCTTC TTCACTTCTC TAAACCCCA
* * * * *
320
TCTGTGTATC TGTACAGGAA TGAATGAATG AGTATGTGCA GCCAAGCTAT GCAAACTCCA GGTTAAAATA TTGCCTTGGG
* * * * *
400
TTTTTTAGTA AATTGTTCAA GCCCATGACA TTCTAGCAGA AAAAGCCTAG TGTCTCTTTC TTAAGGTGAT TGTGTCCATG
* * * * *
480
TGTTTTCCAG GAACTCTATG GGTTCCTCAA CCCAAATTCA CCCTGCCCTT GACCAAATGG CTCACCAGCT TCACGGATGC
* * * * *
560
TGCTCTGATG ACACACCCTG CAGTCAGCAT CTGCCCTGC AGCTAGAATG GATTCTGAG TGGGCATTAG CTGGGGGATA
* * * * *
640
CCACATGGGC ACCAATGTCA CAGATCTTCT GTCACAGTCC ACCCCGAACC ATTGCTTCTC AAATCATAAT CCCTTAGCAG
* * * * *
720
GACAGCTAGG TGCAGCACGC ATGACACAAA CACCAGCCCT TGCCTACAAT CTCAGCCACT ATCTTGAGTC TGAGCAACTA
* * * * *
800
GTCTAGTGGC AGCCGCGCCC TTCCTTTTCA AGAGAGTTCT GGGATCAGAT CCTTTCACAA ACAGATCCCT CCCCACCCTG
* * * * *
880
CCTGTTGTCC AGGTCTGCAC ACTGAAAAGT AAGACAGCAT TTGCTAAGCC ATATTTCAAA AAGTTTGCTT ATACCTTCAT
* * * * *

FIG. 7A

```

                >Af12                                >Stu1
                |                                      |
          *      *      *      *      *      *      *      *      *
CTCAGGACAA CAAGTGCCTG CTTAAGAGCC TTATGTTTGT GTAAGTGGTA TTTTTCCTT CCCTGACCTT CCAAGGCCTA
          *      *      *      *      *      *      *      *      *
          *      *      *      *      *      *      *      *      *
GTCTACTTTC TCCCTCCCTA GCTGAACAAA AGTGAAGTTG AAATAATTG AACTACCCCT TTTAGTGGG AGCCATTG
          *      *      *      *      *      *      *      *      *
          *      *      *      *      *      *      *      *      *
ATTTTACCT TAGCCAGAGC CTTAATTGT CCATGTGAGC ATAGCAGTAC CTTGCAGCAC CTGAGGCACA ATACATTGT

>Dra1
>Aha3
|
          *      *      *      *      *      *      *      *      *
TAAAGAGTGA CAGTGCCTCC CATTCCAATA AGAACCACAC TCAGAGCAAA GGTTCCTCT CCTGTGTGA GAGTGACCCA
          *      *      *      *      *      *      *      *      *
          *      *      *      *      *      *      *      *      *
TGGTAGAAAA TTTGCAGACT TCGTTACCTC TTCATCAGTT GAAAAATCTA TTTATTCATT TATGCATTTA ATTTTCCTA

          *      *      *      *      *      *      *      *      *
          *      *      *      *      *      *      *      *      *
TCTAAGCCAG GGATAGTCAA ACATTTCTG TAAAGGGCCA AGTAGCATGA TAAATATGT AGGCTCTGCA GGCCACTTAC

          *      *      *      *      *      *      *      *      *
          *      *      *      *      *      *      *      *      *
AGTTTTGTCA TGTATTCTTT TTTTGCTCCC TGTTGTATT ATTTGTGTTA CAATGCTTTA AAAATGTAAA AAAACAGATG

          *      *      *      *      *      *      *      *      *
          *      *      *      *      *      *      *      *      *
ATCACTGGAG TCTCAGGGT CCCTCGGGC ACACAGGGAC AAGCAAAGGC TACATCCAGA TACCAGAAAT GCACTGACGC
          *      *      *      *      *      *      *      *      *
          *      *      *      *      *      *      *      *      *
CCGTTCTTGG AAGCTGGGCT CCCACTCAGC CCCTGGGAGC AGCAGCCTCC AGCCCTTGG GACCTTCAAC TCCACCCTGC
          *      *      *      *      *      *      *      *      *
          *      *      *      *      *      *      *      *      *
TGACCCACGC GGGTTGAGCC AGCATCCCTG GAGGCTGACA CTGTCCTCCA CTGAGACCTG AAAA ATG GCA TCG GGG
          *      *      *      *      *      *      *      *      *
          *      *      *      *      *      *      *      *      *
M A S G>

```

FIG. 7B

SUBSTITUTE SHEET (RULE 26)

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1680
 * * * * *
 CAA GGC CCA GGG CCT CCC AGG CAG GAG TGC GGA AAG CCT GCC CTG CCC TCT GCT TCT GAG GAG CAG
 Q G P G P P R Q E C G K P A L P S A S E E Q>

1760
 * * * * *
 GTA GCC CAG GAC ATG GAG GGG TTT TCC GCA GCT ACG TTT TTT ACC ACC ATC AGC AGG AAC AGG AGG
 V A Q D M E G F S A A T F F T T I S R N R R>

>Not1
 * * * * *
 CTG AAG GGG CGG CCG CCC CTG CCG ACC CAG AGA TGG TCA CCT TGC CCC TCC AAC CTA GCA GCA CCA
 L K G R P P L P T Q R W S P C P S N L A A A P>

1840
 * * * * *
 TGG GGC AGG TGG GAC GGC AGC TCG CCA TCA CCA GGA CGA CAT CAA CCG GCA CTA TGA CTTGCGAGT
 W G R W D G S S P S P G R H Q P A L *>

1920
 * * * * *
 TCCAGACCAT GCTGCAGCAC CTGCAGCCCA CGGCAGAGAA CGCCTACGAG TACTTCACCA AGATCGCCTC CAGCCTGTTT

>Pst1 >Pst1 >Sca1
 * * * * *
 GAGAGTGGCA TCAACCGGG CCGTGTGGTG GCTCTCCTGG GCTTCGGCTA CCGTCTGGTC CTACATGTCT ACCAGCACGG

2000
 * * * * *
 CTTGACTGGC TTCCTGGGCC TGGTGACCCG CTTCTGGTTC TTCATGCTGC AACAAGGCAT CGCCCGGTGG ATCTCGCAGA

2080
 * * * * *
 GGGGCGGCTG GGTGGCAGCC CTGGACTTGG GCAATAGTCC CATCCTGAAC GTGCTGGTGG TTGTGGGTGT GGTTCGTCTG

2160
 * * * * *
 GGGGCGGCTG GGTGGCAGCC CTGGACTTGG GCAATAGTCC CATCCTGAAC GTGCTGGTGG TTGTGGGTGT GGTTCGTCTG

2240
 * * * * *
 GGGGCGGCTG GGTGGCAGCC CTGGACTTGG GCAATAGTCC CATCCTGAAC GTGCTGGTGG TTGTGGGTGT GGTTCGTCTG

>Pvu2
 * * * * *
 GGGGCGGCTG GGTGGCAGCC CTGGACTTGG GCAATAGTCC CATCCTGAAC GTGCTGGTGG TTGTGGGTGT GGTTCGTCTG

2320
 * * * * *
 GGGGCGGCTG GGTGGCAGCC CTGGACTTGG GCAATAGTCC CATCCTGAAC GTGCTGGTGG TTGTGGGTGT GGTTCGTCTG

>Af12
 * * * * *
 GACTTAAGCC AAGTCTTTGC CTTCCCACT CCCTTGACAG GGTACCCCTT CAAAAGTACA GAAGCTCTAG CAAGTGTGCA

2400
 * * * * *
 GACTTAAGCC AAGTCTTTGC CTTCCCACT CCCTTGACAG GGTACCCCTT CAAAAGTACA GAAGCTCTAG CAAGTGTGCA

FIG. 7C

SUBSTITUTE SHEET (RULE 26)

SUBSTITUTE SHEET (RULE 26)

3440
* * * * *
CAGTGTGGGG GTGAGAGTAC CTTCTCTATC GGGCACAGCC TAGGGTGTG GGGGTGAAGG GGGAGAAGTT CTTGATTCAG

3520
* * * * *
CCAAATGCAG GGAGGGGAGG CAGAAGGAGC CCACAGGCCA CTCCTATCC TCTGAGTGT TGGAAATAAA CTGTGCAATC

3600
* * * * *
CCATCAAAAA AAAAAAGGAG AAAAAATGT AAAAAACATT CTTAGCTGTA AGCTACTTAT AGGGGGATAA AGACAGGACT

3680
* * * * *
GTTAATGGAC ACAACATAC AGTTAGAGAG AAGAAATAAG TTCTGTCCAG GCACGGTGCC TCACACCTCT AACTCCAGCA

>Bg12
|
3760
* * * * *
CTTTGGGAGA CCAAAGTGGG AAGATCATT GAGTCCAGGA GTTCGAGACC AGCCTGGACA ACATAGCAAG ATCTTATCTC

>Dra1
|
>Aha3
|
3840
* * * * *
TACAGAAAAT TTAAAAAAA GAAAAAACT AGCCGCACAG GTCTGCAGTC CTAGCTACTC GGGAGGCTAA GGTGGGAGAA

>Pst1
|
3920
* * * * *
TCCTTGAACC CAGGGATTGA GTTTGAGGTT GCAGTGAGCT ATGATTGCAC CACTGCACTC CAGACTGGGT GACTGAGTGA

4000
* * * * *
GACCCTGTCT CAAATATAAA GAAGGAACAA GTTCTAGTTT TCAATAGCGC AATAGGGTGA GTGCAGTTAG CAACAACATA

4080
* * * * *
TTGTGTATTT CAAAATAGCT ACAAGAGAGG ATATGAAGTG TTCCCCAAA CAAGGAATGA TAACGTTCSA GGTGACAGAT

4160
* * * * *
ACCTTAAATA CCCTGATTG ATCATTACAC ATTCAATGTA TGTATCAAAA TATTACATGT ACCCCACAAA TTTGTGTAAA

>Dra1
|
>Aha3
|
4240
* * * * *
TATTATGTAT CCACTTTTGA AAGTTGGCAG AGCCCAAAAG CACTACTATG GCTTCCAGTG GTCACTGTGA GCACTGCCAG

FIG. 7E

SUBSTITUTE SHEET (RULE 26)

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4320
* * * * *
CTCAGCAAAT GTATCACCCA AAATCTGGGC AATGTGGGAA ATTGGCTTCA TGGCAGCTAT GGCTTTGCCA CTGATAGGAA

>Bcl1
|
4400
* * * * *
TGATTTCAG AGATACTTAA TCCTCAATTC GGGACTCTTT GCTTCAGGAG TTTGGCTGGC CAGGAACATG AGTGACAGTG

>Pvu2 >Xba1
| |
4480
* * * * *
ACCTCTTGGC ACTTCAGCTG GGGGTGTAGC CAAGCAGACA AATGGAATCT TGTGCTGAAC CCAAACCTTC TAGAAACAGA

>Pvu2
|
4560
* * * * *
GCCTGTGAGC ATCACAAGAT ATGCCCTGAT GGAAGCTGAA GTTTAATTCA GCTGAGCGCT TGCCCTTTC CAACCTGGTT

>Bcl1
|
4640
* * * * *
TCCTTTTGT CTTGAGTCC AGTCAGAATG CCATTCCCTG GCCAGCAGCC AGCCTTAGT GACTGTCTCT GTTCTGCAAA

>Pst1
|
4720
* * * * *
GCTCTGTATA TAGTTACTGA GTTCTGCAG GGGGTGATCT TTGCTCTGT CCTAAGAAAT AACTACAGTG TTTTAAGAAA

4800
* * * * *
TATTTGAGGC CGGGTGCAGT GGTTACACCC TGTAATCCAG CACTTTGGGA GGCCAAGGCA GGTGGATCAT GAGGTCAAGA

>Bcl1
|
4880
* * * * *
GTTTGAGACC ATCATGGCCA ACATGGTGAA ACCCATCTC TACTAAAAAT AAAAAATTA GCTGGGTGTG GTGGCGGGCA

>EcoR5
|
4960
* * * * *
CCTGTAGTCC CAGCTACTCG GGAGGCTGAG GCAGGAGAAT CGCTTGAGCC TGGGAGGCGG AGGTTGCACT GAGCCGATAT

FIG. 7F

SUBSTITUTE SHEET (RULE 26)

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5040
CACGCCACTG CACTCCAGCC TGGCGACAGA GCGAGACTCC ATCTCAAAAA AAAGAAAAAA TAAATAGTTG AAATAAGAC
* * * * *
5120
TGCACATAAA GACAAAAAAA AAGTTTATAA AGTTAAAAAA TAAATAAAAA AACAGGCTCC AGGCTGGATT GGGCCCAGAG
* * * * *
5200
GCTGTAGGAC ACAGACCCCC AGCCAATGAC TTCATAAATC CGGATGTAA TCAGCCTCAC CTGGGAATTT GGGGAGGGGA
* * * * *
5280
CTCATTTTAA AACAGTTTCC TGGATTCTAA CCCAACCAG AAAATCAGAC TCTTTGAGCT AAATTCTTAA GCTCCCTGGT
* * * * *
5360
GATGATGATG GAACCAGTTT ATGGCTGACC CCAGAGTACC GTCTGAAAGA CGTGCCACAT CCCTCTCTCT CCAGCCTCCC
* * * * *
CTTCTCCTCC ATTCCCAGG GAGAATTC
* * * * *

>Aha3
|
>Dra1
|
>Afl2
|
>EcoR1
|

FIG. 7G

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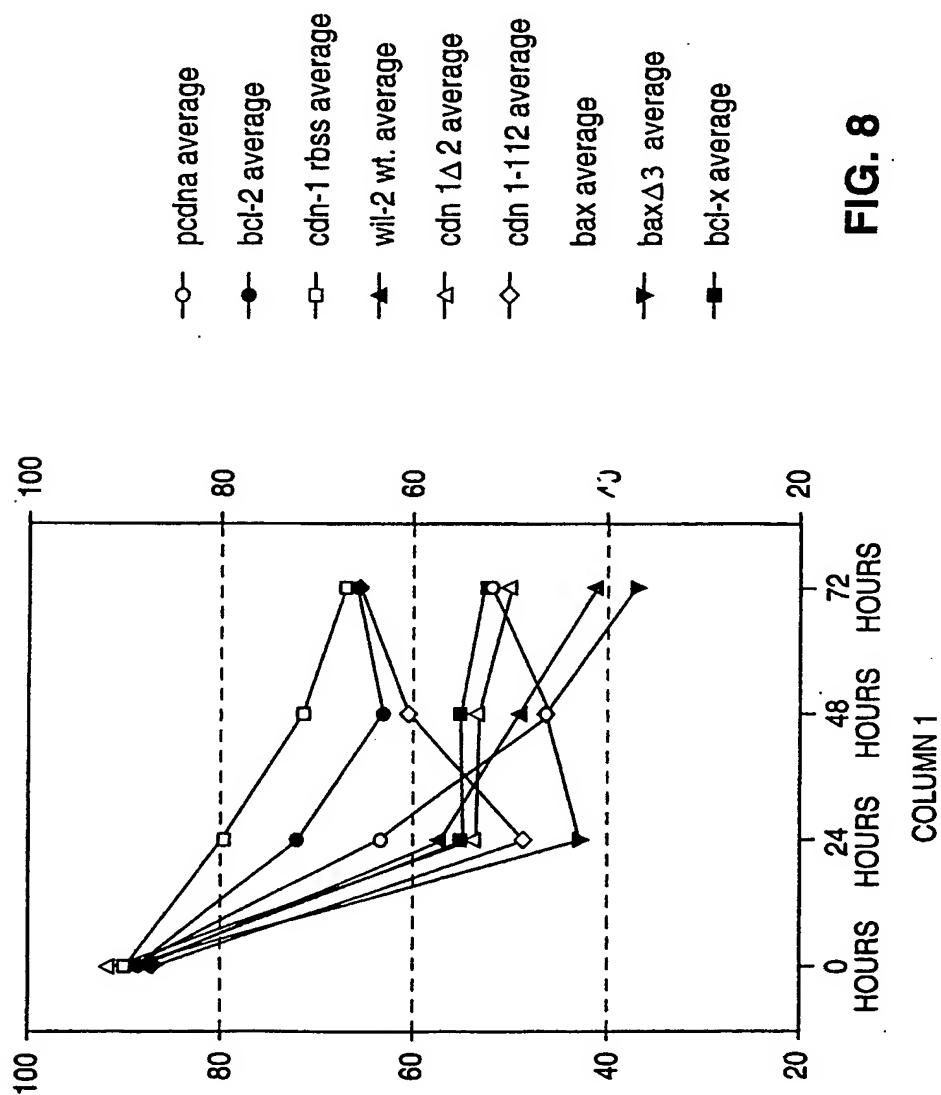


FIG. 8

RECTIFIED SHEET (RULE 91)

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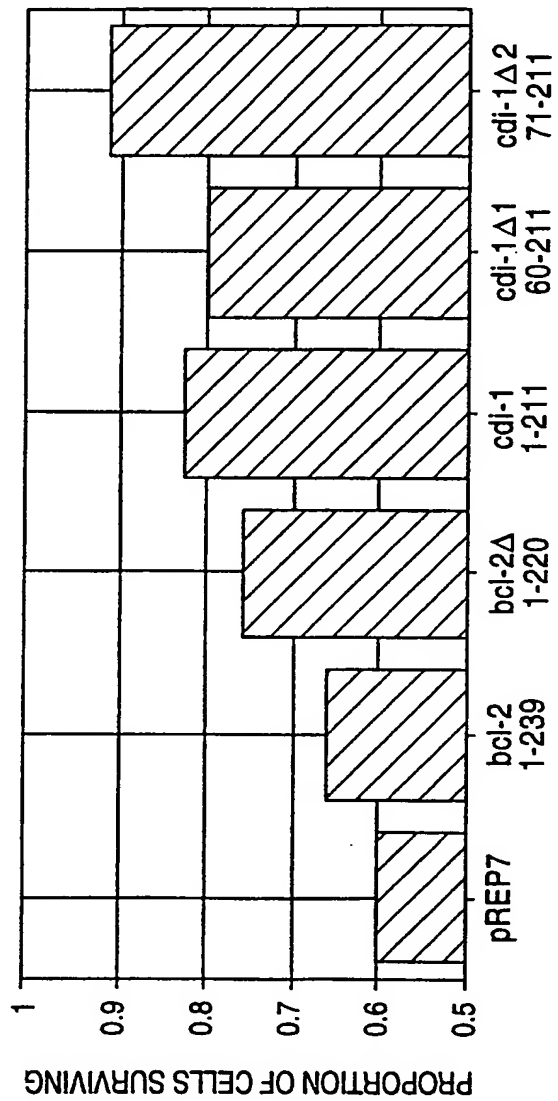
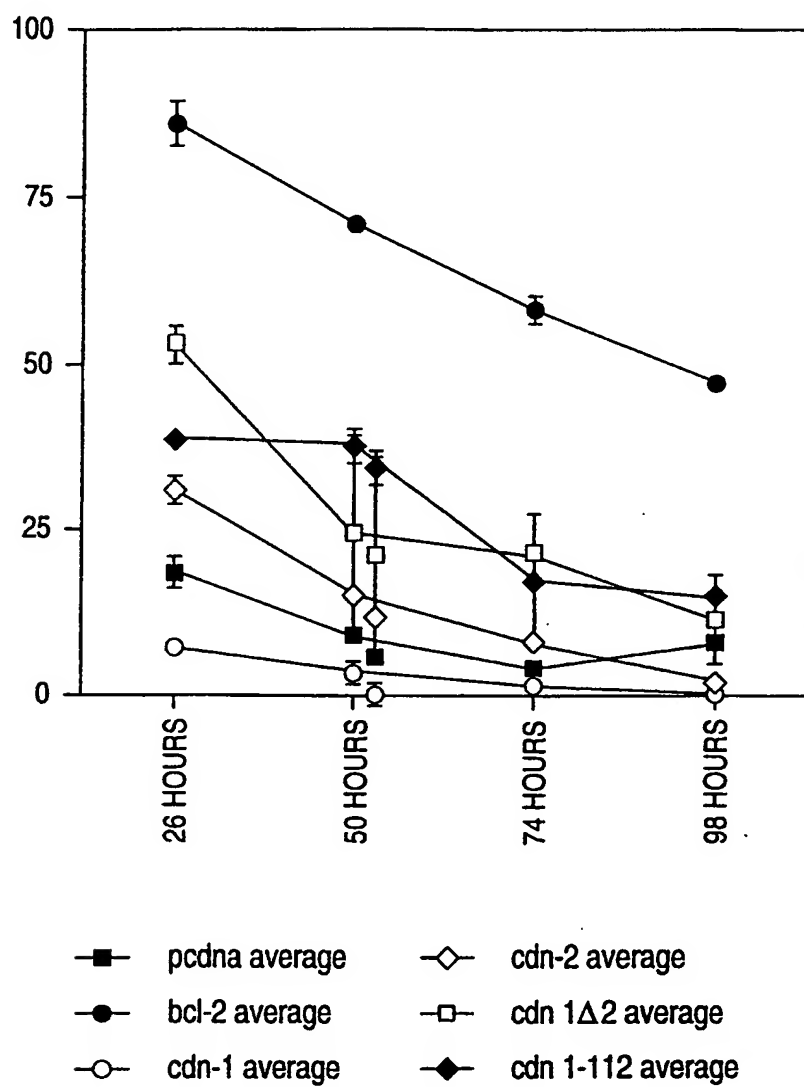


FIG. 9

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**FIG. 10**

SUBSTITUTE SHEET (RULE 26)

MASGQGP^{Δ1}PPRQECGEPALPSASEEQVAQDTEEVFRSYVFYRHQQEQEAEGVAAPADPEMVT
LPLOPSST^{Δ2}MGQVGRQLAIIGDDINRRYDSEFQTMLQH^{Δ3}LQPTAENAYEYFTKIATSLFESGNWGR
VVALLGFGYRLALHVVYQHGLTGFLGQVTRFVVDFMLHHCIARWIAQRGGWVAALNLGNGPILN
VLVVLGVVLLGQFVRRFFKS

FIG. 11

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US94/13930

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : Please See Extra Sheet.

US CL : Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 424/93.21, 130.1, 141.1; 435/6, 7.1, 7.2, 7.21, 7.24, 7.7, 7.8, 69.1, 70.1, 240.21, 320.1; 514/2, 44; 530/387.1; 800/2

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	CELL, Volume 74, issued 27 August 1993, L.H. Boise et al., "bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic cell death", pages 597-608, see entire document.	1-61
Y	CELL, Volume 74, issued 27 August 1993, Z.N. Oltvai et al., "Bcl-2 heterodimers in vivo with a conserved homolog, Bax, that accelerates programmed cell death", pages 609-619, see entire document.	1-61
Y	SCIENCE, Volume 261, issued 09 July 1993, N. Zhu et al., "Systemic gene expression after intravenous DNA delivery into adult mice", pages 209-211, see entire document.	42-58

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	X	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	Y	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	G	document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means		
P document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

07 MARCH 1995

Date of mailing of the international search report

20 MAR 1995

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Commissioner of Patents and Trademarks
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Washington, D.C. 20231

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BRIAN R. STANTON

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US94/13930

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	CELL, Volume 74, issued 10 September 1993, G.T. Williams et al., "Molecular regulation of apoptosis: genetic controls of cell death", pages 777-779, see entire document.	1-61
Y	CELL, Volume 75, issued October 1993, D.M. Hockenberry et al., "Bcl-2 functions in an antioxidant pathway to prevent apoptosis", pages 241-251, see entire document.	1-61
Y	BIO/TECHNOLOGY, Volume 11, issued 11 July 1993, S.M. Edgington, "Looking death in the eye: Apoptosis and cancer research", pages 787-792, see entire document.	1-61
Y	CELL, Volume 67, issued 29 November 1991, A. Strasser et al., "bcl-2 transgene inhibits T cell death and perturbs self-censorship", pages 889-899, see entire document.	1-61
Y	CELL, Volume 67, issued 29 November 1991, C.L. Sentman et al., "bcl-2 inhibits multiple forms of apoptosis but not negative selection in thymocytes", pages 879-888, see entire document.	1-61
Y	CELL, Volume 47, issued 10 October 1986, M.L. Cleary et al., "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin transcript resulting from the t(14;18) translocation", pages 19-28, see entire document.	1-61
Y	IMMUNOLOGY TODAY, Volume 12, number 4, issued 1991, J.C. Ameisen et al., "Cell dysfunction and depletion in AIDS: the programmed cell death hypothesis", pages 102-105, see entire document.	1-61

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US94/13930

A. CLASSIFICATION OF SUBJECT MATTER:

IPC (6):

A01N 43/04, 63/00; A6HK 31/70, 37/00; C07K 16/00, 16/18; C12N 1/08, 1/21, 5/00, 5/06, 5/16, 7/00, 15/09, 15/13

A. CLASSIFICATION OF SUBJECT MATTER:

US CL :

424/93.21, 130.1, 141.1; 435/6, 7.1, 7.2, 7.21, 7.24, 7.7, 7.8, 69.1, 70.1, 240.21, 320.1; 514/2, 44; 530/387.1; 800/2

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

Databases: APS, CA, BIOSIS, MEDLINE, EMBASE, DERWENT, USPATFULL, SCISEARCH

Search Terms: apoptos?; bcl?; cdn?; cdi?; protein?; cdna; dna?; antibod?; transgen?; polyclon?; monoclon?; T (w) cell?; lymphocyt?; immun?; northern?; elisa; pcr; polymerase chain reaction; gene; therapy; ex vivo; in vivo; superoxide; dismutase; sod?; yeast

XX WPI; 1996-139648/14.
 DR P-PSDB; AAR81451.
 XX New isolated human Bcl-Y protein - used to develop prods. for treating
 PT disorders characterised by inappropriate cell proliferation or cell
 PT death.
 XX Claim 6; Fig 4; 100pp; English.
 PS A full-length cDNA clone (AAR81451) codes for Bcl-Y (AAR81451), a protein
 CC that induces apoptosis in cells and functions as a negative regulator of
 CC Bcl-2 function. It was isolated from a Jurkat cell cDNA library using as
 CC probe a partial Bcl-Y cDNA clone obtd. by PCR of DNA derived from the
 CC Namalwa cell line. The cDNA can be used for prodn. of recombinant Bcl-Y,
 CC as a probe, to produce transgenic animal models, and in the gene therapy
 CC of disorders characterised by inappropriate cell proliferation or cell
 CC death
 XX
 XX Sequence 1968 BP; 382 A; 560 C; 576 G; 450 T; 0 U; 0 Other;
 SQ
 Query Match 43.9%; Score 1013; DB 2; Length 1968;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1353; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 953 GGTGACGCGCTGAACTTGGGCAATGTCCATCTCCATCTGAACTGCTGGTGTCTGGTGT 1012
 995 GGTGGCAGCCCTGAACTTGGGCAATGTCCATCTCCATCTGAACTGCTGGTGTCTGGTGT 654
 1013 GGTGCTGTGGGCAATGTGGTACGAAGATTTCTTCAAATCATGACTCCCAAGGGTGC 1072
 655 GGTGCTGTGGGCAATGTGGTACGAAGATTTCTTCAAATCATGACTCCCAAGGGTGC 714
 1073 CTTTGGGCTCCGGTTGACAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1132
 715 CTTTGGGCTCCGGTTGACAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 773
 1133 CTTTGGGCTCCGGTTGACAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1192
 774 CTTTGGGCTCCGGTTGACAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 833
 1193 GAGAGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1252
 834 GAGAGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 893
 1253 AGTGGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1312
 894 AGTGGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 953
 1313 CTCCTTAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1372
 954 CTCCTTAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1013
 1373 GAGAGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1432
 1014 GAGAGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1073
 1433 AGCCATTTCCCACTTCTACCTGAGGCGCAGGAGCTGCTGGGCTGGGCTGGGCTGGGCT 1492
 1074 AGCCATTTCCCACTTCTACCTGAGGCGCAGGAGCTGCTGGGCTGGGCTGGGCTGGGCT 1133
 1493 TATGTTTCCCGAGATTCAGCTATTCTGGAAGATCAGACCTCAGACCTAAGAGATGGGCTAGG 1552
 1134 TATGTTTCCCGAGATTCAGCTATTCTGGAAGATCAGACCTCAGACCTAAGAGATGGGCTAGG 1193
 1553 CTGAGCTTGGTCTGGCGCTCCCTAAGCATGTGTCCTGAGGAGGAGGAGCTTACTAGGAGAG 1612
 1194 CTGAGCTTGGTCTGGCGCTCCCTAAGCATGTGTCCTGAGGAGGAGGAGCTTACTAGGAGAG 1253
 1613 GGGGGCCAGGCTCTGCTCAACTCTACCCCTGCTCCCAATCTCTCTCTCTCTCTCTCTCTCT 1672
 1254 GGGGGCCAGGCTCTGCTCAACTCTACCCCTGCTCCCAATCTCTCTCTCTCTCTCTCTCTCT 1313

QY 1673 CTTTGCAGTGGAGTCTCTCAGGGATTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 1732
 DB 1314 CTTTGCAGTGGAGTCTCTCAGGGATTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 1373
 QY 1733 ACCAGAGCTGTCTGAACTCAGCTGTGAGAAAGCTTCCAGCTTCCCTCCCAAGGCTCTCTC 1792
 DB 1374 ACCAGAGCTGTCTGAACTCAGCTGTGAGAAAGCTTCCAGCTTCCCTCCCAAGGCTCTCTC 1433
 QY 1793 AGTTCT 1852
 DB 1434 AGTTCT 1493
 QY 1853 AGGCTCTCAACCCCT 1912
 DB 1494 AGGCTCTCA-CCCATCT 1552
 QY 1913 CCAGACTACAGGCTTAGGCTTGGTGTGTTTATTTTCAAGGAAAGAGGTAGGAGTTTCAT 1972
 DB 1553 CCAGACTACAGGCTTAGGCTTGGTGTGTTTATTTTATATCAGGAAAGAGGTAGGAGTTTCAT 1612
 QY 1973 CTGAGGCTTCTAAGTGGGAGAGGACTATCAACACACCTAGGAATCCAGAGTGGGAT 2032
 DB 1613 CTGAGGCTTCTAAGTGGGAGAGGACTATCAACACACCTAGGAATCCAGAGTGGGAT 1672
 QY 2033 CTTCTCTATGCTCTGCGCAGAGTGTATCCAGGGGTAGATGGGGGAACTGTCAATAC 2092
 DB 1673 CTTCTCTATGCTCTGCGCAGAGTGTATCCAGGGGTAGATGGGGGAACTGTCAATAC 1732
 QY 2093 TTGAATCT 2152
 DB 1733 TTGAATCT 1792
 QY 2153 GGTGACAGTCT 2212
 DB 1793 GGTGACAGTCT 1852
 QY 2213 TCTTGAATCTAGCCAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2272
 DB 1853 TCTTGAATCTAGCCAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1912
 QY 2273 CTCTGAGTGTGTTGGAATTAAGTGTGCAATCCCTCA 2309
 DB 1913 CTCTGAGTGTGTTGGAATTAAGTGTGCAATCCCTCA 1949
 RESULT 3
 AAQ95492
 ID AAQ95492 standard; cDNA; 2072 BP.
 XX AC AAQ95492;
 XX XX
 DT 25-MAR-2003 (revised)
 DT 21-NOV-1995 (first entry)
 XX XX
 DE Human Cdn-1 cDNA.
 XX Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock;
 KW lymphoma; eczema; ss.
 XX OS
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH CDS 188..903
 FT /*tag= a
 FT
 XX W09515084-A1.
 XX PN
 XX PD 08-JUN-1995.
 XX PF 30-NOV-1994; 94WO-US013930.
 XX PR 30-NOV-1993; 93US-00160067.

PR 07-OCT-1994; 94US-00320157.
 XX (LXRB-) LXR BIOTECHNOLOGY INC.
 PA Kiefer MC, Barr PJ;
 XX WPI; 1995-215106/28.
 DR P-PSDB; AAR77876.
 DR New nucleic acid sequences encoding Cdn apoptosis modulators - and
 XX related vectors, transformed cells, proteins and antibodies, useful for
 PT diagnosis and treatment e.g. of HIV infection, reperfusion injury etc.
 PT Claim 4; Fig 3A-C; 66pp; English.
 XX Cdn-1 cDNA was isolated from a human heart cDNA library using a
 CC previously isolated clone as probe. Recombinant Cdn-1 was produced in Sf9
 CC and human colon adenocarcinoma HT29 cells. Expression of Cdn-1 in WI-L2
 CC lymphoblastoid cells resulted in increased cell survival in response to
 CC anti-Fas-mediated apoptosis. (Updated on 25-MAR-2003 to correct EN
 CC field.)
 XX Sequence 2072 BP; 404 A; 603 C; 598 G; 467 T; 0 U; 0 Other;
 SQ Query Match 26.8%; Score 619; DB 2; Length 2072;
 Best Local Similarity 100.0%; Pred. No. 2.2e-287;
 Matches 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 GGACCTCCATCTCCACCTCTGAGCCACCGGGTTGGCCAGGATCCCGAGGCTGAT 271
 DB |||||
 QY 103 GGACCTCCATCTCCACCTCTGAGCCACCGGGTTGGCCAGGATCCCGAGGCTGAT 162
 DB |||||
 QY 272 CCGCTCTCCATCTGAGACCTGAAATATGCTTCGGGGCAAGCCAGGCTCTCCAGGCA 331
 DB |||||
 QY 163 CCGCTCTCCATCTGAGACCTGAAATATGCTTCGGGGCAAGCCAGGCTCTCCAGGCA 222
 DB |||||
 QY 332 GGAGTGGGAGAGCTGCGCTCTGCTCTGAGGAGGAGGTAGCCAGGACACAGA 391
 DB |||||
 QY 223 GGAGTGGGAGAGCTGCGCTCTGCTCTGAGGAGGAGGTAGCCAGGACACAGA 282
 DB |||||
 QY 392 GGAGGTTTTCGAGCTACGTTTTCACGCCATCAGCAGGACGAGGCTGAGGGGT 451
 DB |||||
 QY 283 GGAGGTTTTCGAGCTACGTTTTCACGCCATCAGCAGGACGAGGCTGAGGGGT 342
 DB |||||
 QY 452 GGCTGCCCTCTGCCACCCAGAGATGGTCACTTACCTCTGCAACCTAGCAGCACCATTGG 511
 DB |||||
 QY 343 GGCTGCCCTCTGCCACCCAGAGATGGTCACTTACCTCTGCAACCTAGCAGCACCATTGG 402
 DB |||||
 QY 512 GCAGGTGGAGCGGAGCTCGCCATCATCGGGGAGGACATCAACCGAGCTATGACTCAGA 571
 DB |||||
 QY 403 GCAGGTGGAGCGGAGCTCGCCATCATCGGGGAGGACATCAACCGAGCTATGACTCAGA 462
 DB |||||
 QY 572 GTTCCAGACCATGTTGACGACCTGCGACCCACCGCAGAGAAATGCTATGACTATTAC 631
 DB |||||
 QY 463 GTTCCAGACCATGTTGACGACCTGCGACCCACCGCAGAGAAATGCTATGACTATTAC 522
 DB |||||
 QY 632 CAGATTGTCACGACCTGTTGAGAGTGCATCAATGGGCGCTGTTGGCTCTTCT 691
 DB |||||
 QY 523 CAAGATTGTCACGACCTGTTGAGAGTGCATCAATGGGCGCTGTTGGCTCTTCT 582
 DB |||||
 QY 692 GGCGTTCCGCTACCGCTCTGGCCCTACACGCTTACAGCATGCGCTGCTTCCTAGG 751
 DB |||||
 QY 583 GGCGTTCCGCTACCGCTCTGGCCCTACACGCTTACAGCATGCGCTGCTTCCTAGG 642
 DB |||||
 QY 752 CCAGGTGACCGCTTCTGGTGGTGGCTGATCTGCTGATCTGCTGCTGCTGCTGCTGCT 811
 DB |||||
 QY 643 CCAGGTGACCGCTTCTGGTGGTGGCTGATCTGCTGATCTGCTGCTGCTGCTGCTGCT 702
 DB |||||
 QY 812 ACAGAGGGGTGGCTGGGTG 830
 DB |||||
 QY 703 ACAGAGGGGTGGCTGGGTG 721
 DB |||||

RESULT 4
 AAT42138
 ID AAT42138 standard; cDNA; 2094 BP.
 XX
 AC AAT42138;
 XX
 DT 22-FEB-1997 (first entry)
 XX
 DE Bak gene.
 XX Human; Bak; apoptosis; latency; virus replication; Epstein-Barr virus;
 KW BHRF1; fusion protein; epitope tag; drug screening; co-precipitation;
 KW ELISA; immunosay; antibody; protein interactive trapping; virucide;
 KW antitumour; diagnostic; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 5'UTR 1..200 /tag= a
 FT CDS 201..836 /tag= b
 FT 3'UTR /product= "Bak protein"
 FT 837..2094 /tag= c
 FT
 FT WO9633416-A1.
 XX
 XX 24-OCT-1996.
 XX
 XX 19-APR-1996; 96WO-US005639.
 XX
 XX 20-APR-1995; 95US-00426529.
 XX (LXRB-) LXR BIOTECHNOLOGY INC.
 XX
 XX Barr PJ, Kiefer MC;
 XX WPI; 1996-485886/48.
 DR P-PSDB; AAR03668.
 DR
 XX Screening for anti-viral agents - by detecting the ability of an agent to
 PT disrupt the interaction of a Bak protein and a viral protein.
 PT
 XX Disclosure; Fig 1; 24pp; English.
 XX
 XX The sequence encodes Bak protein, which is a bcl-1 homologue which
 CC interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein,
 CC and is capable of modulating apoptosis. The Bak gene is located on human
 CC chromosome-6 at 6p21-23. The protein may be used in complete or partial
 CC form, or as an epitope tag fusion protein, in a new virucide drug
 CC screening method, which involves combination of Bak protein and a viral
 CC protein (e.g. EBV BHRF1), exposure to a test compound, and monitoring for
 CC disruption of the interaction, e.g. by co-precipitation, protein
 CC interactive trapping or ELISA. Interaction of Bak and viral proteins
 CC allows viral replication or latency in the absence of apoptosis.
 CC Compounds which inhibit the interaction may be used as virucide,
 CC antitumour or diagnostic agents
 XX
 XX Sequence 2094 BP; 410 A; 608 G; 470 T; 0 U; 0 Other;
 SQ Query Match 26.8%; Score 619; DB 2; Length 2094;
 Best Local Similarity 100.0%; Pred. No. 2.2e-287;
 Matches 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 GGACCTCCATCTCCACCTCTGAGCCACCGGGTTGGCCAGGATCCCGAGGCTGAT 271
 DB |||||
 QY 116 GGACCTCCATCTCCACCTCTGAGCCACCGGGTTGGCCAGGATCCCGAGGCTGAT 175
 DB |||||
 QY 272 CCGCTCTCCATCTGAGACCTGAAATATGCTTCGGGGCAAGCCAGGCTCTCCAGGCA 331
 DB |||||
 QY 176 CCGCTCTCCATCTGAGACCTGAAATATGCTTCGGGGCAAGCCAGGCTCTCCAGGCA 235
 DB |||||

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